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**Ting et al.**

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(54) **COMPOSITION FOR PROMOTING  
CARTILAGE FORMATION OR REPAIR  
COMPRISING A NELL GENE PRODUCT AND  
METHOD OF TREATING  
CARTILAGE-RELATED CONDITIONS USING  
SUCH COMPOSITION**

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This patent is subject to a terminal disclaimer.

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**Related U.S. Application Data**

(60) Division of application No. 11/594,510, filed on Nov. 7, 2006, now Pat. No. 7,687,462, which is a continuation-in-part of application No. 10/527,786, filed as application No. PCT/US03/029281 on Sep. 15, 2003, now abandoned, said application No. 11/594,510 is a continuation-in-part of application No. 10/544,553, filed as application No. PCT/US2004/003808 on Feb. 9, 2004, now Pat. No. 7,544,486, said application No. 11/594,510 is a continuation-in-part of application No. PCT/US2006/005473, filed on Feb. 16, 2006, said application No. 11/594,510 is a continuation-in-part of application No. 11/392,294, filed on Mar. 28, 2006, now Pat. No. 7,776,361.

(60) Provisional application No. 60/410,846, filed on Sep. 13, 2002, provisional application No. 60/445,672, filed on Feb. 7, 2003, provisional application No. 60/653,722, filed on Feb. 16, 2005.

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**A61K 38/17** (2006.01)

**A61K 38/18** (2006.01)

(52) **U.S. Cl.** ..... **514/17.1; 514/17.2; 514/1.1; 514/7.6; 424/422; 424/423**

(58) **Field of Classification Search** ..... None  
See application file for complete search history.

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(57) **ABSTRACT**

Provided herein are a composition for promoting cartilage formation or regeneration comprising a NELL gene product and a method of treating cartilage-related conditions using such a composition.

**27 Claims, 11 Drawing Sheets**

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Normal cartilage

Nell-1 overexpression  
cartilage

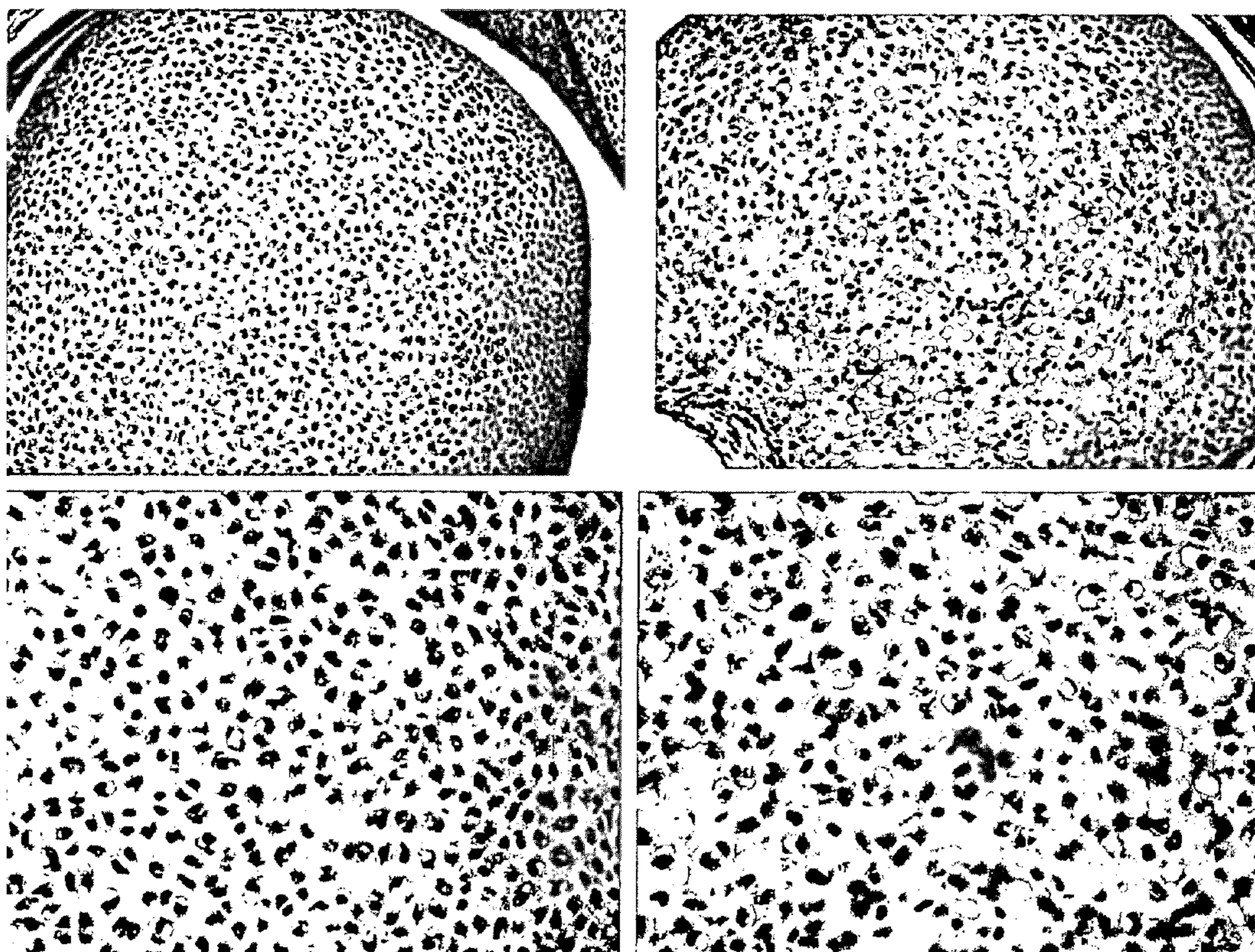


Figure 1

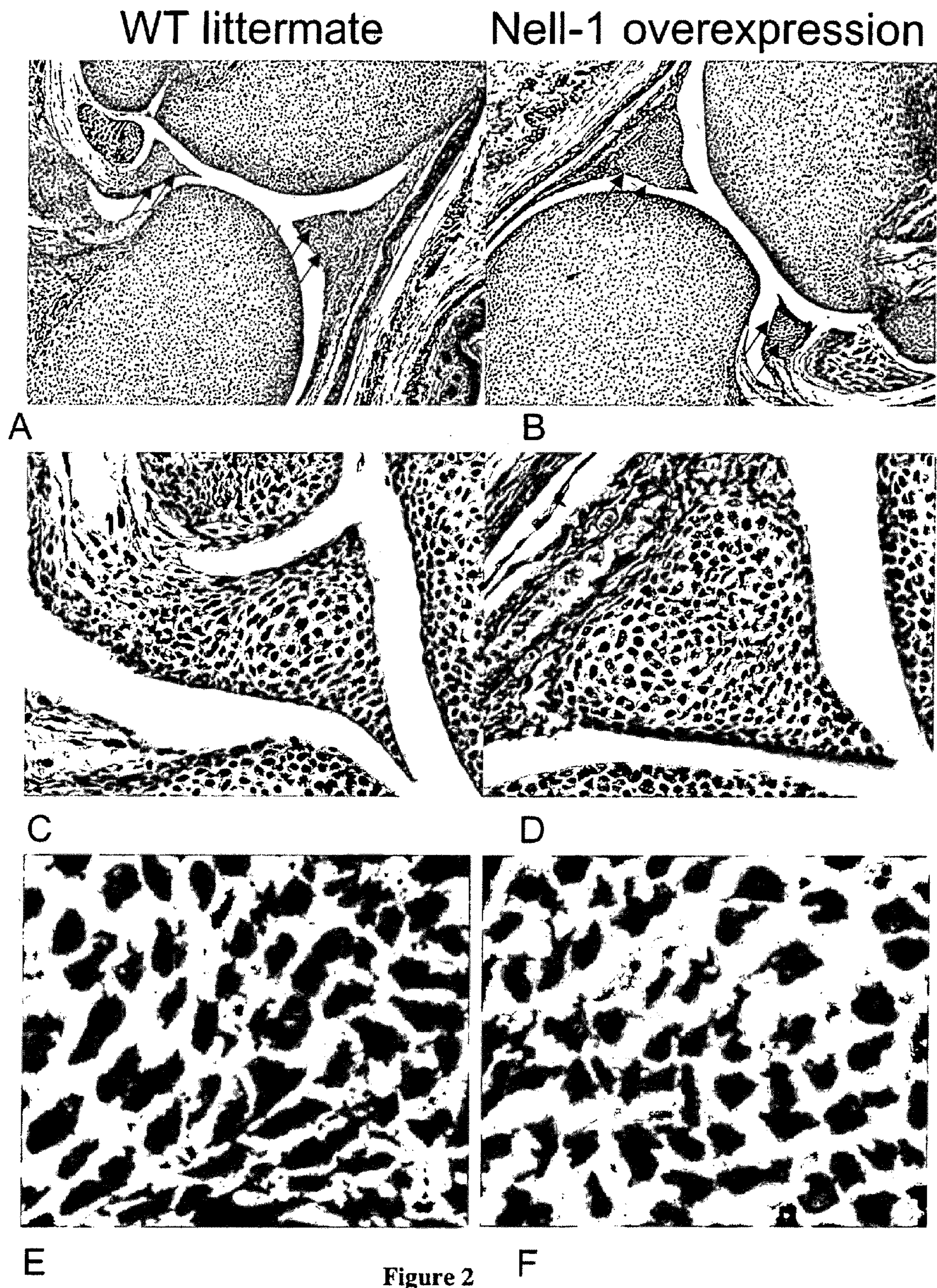


Figure 2

A

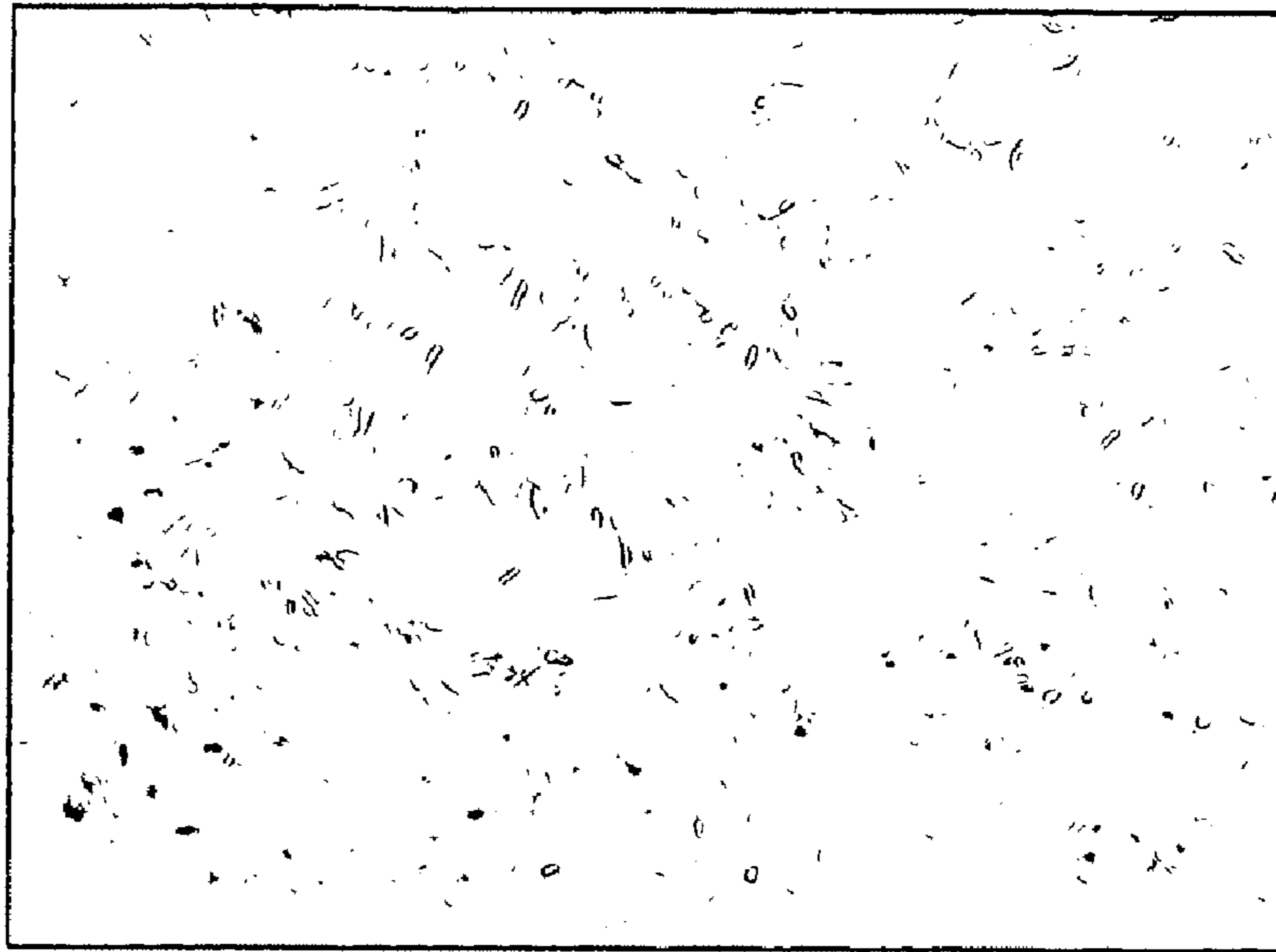


Figure 3A

B

AdNell-1

AdBMP-2

AdLacZ

Nell-1



actin



Figure 3B

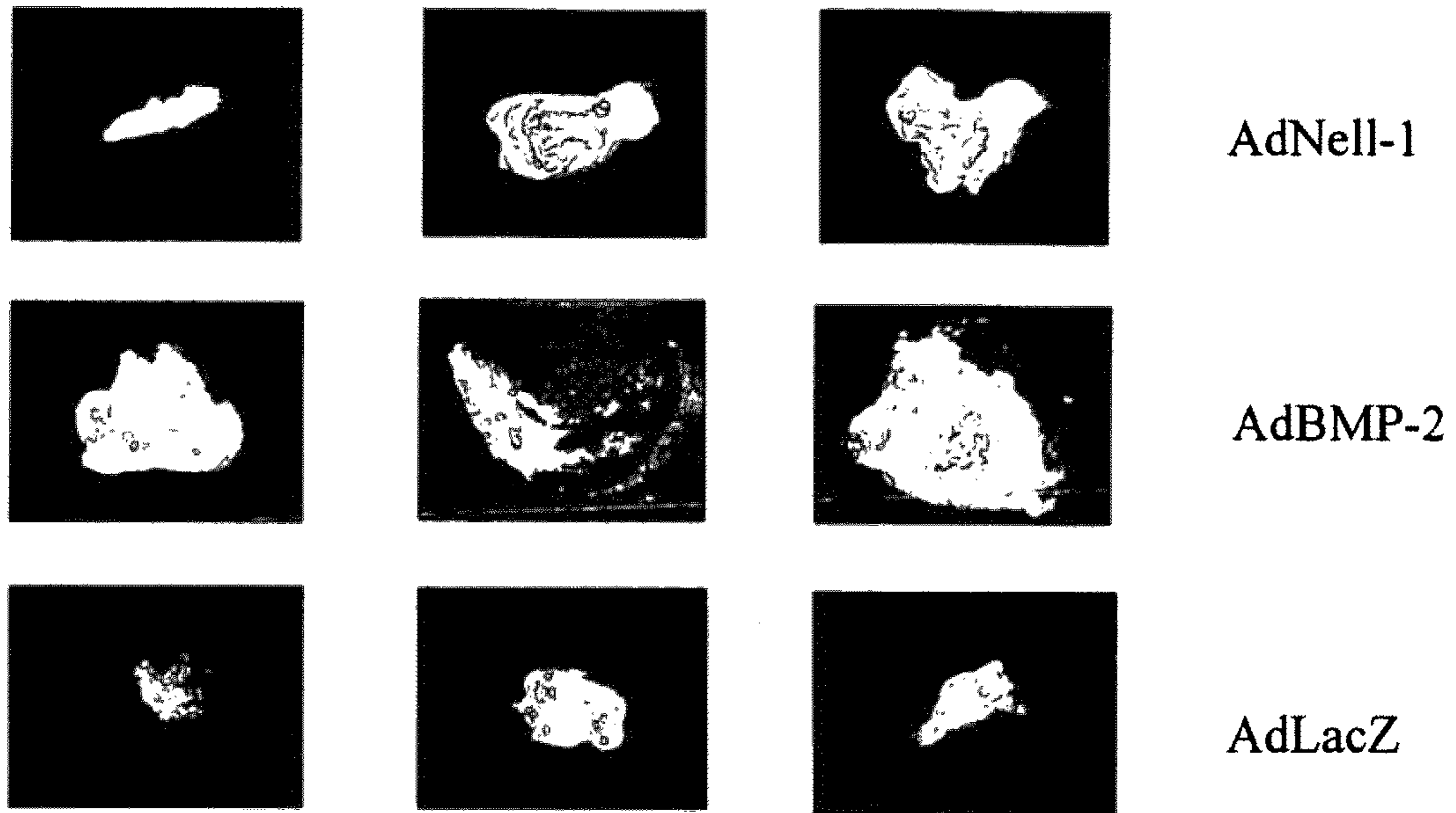


Figure 4A

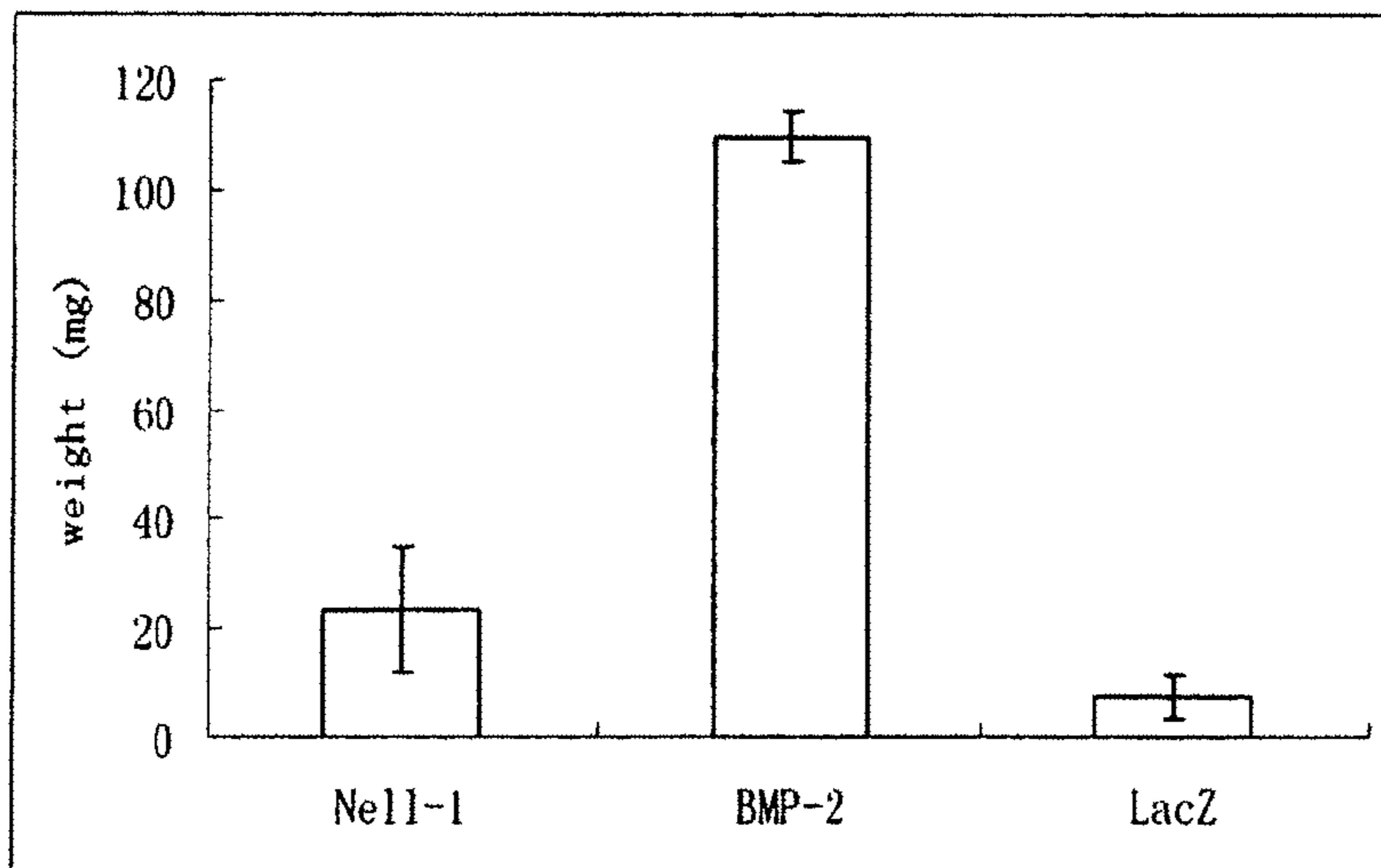


Figure 4B

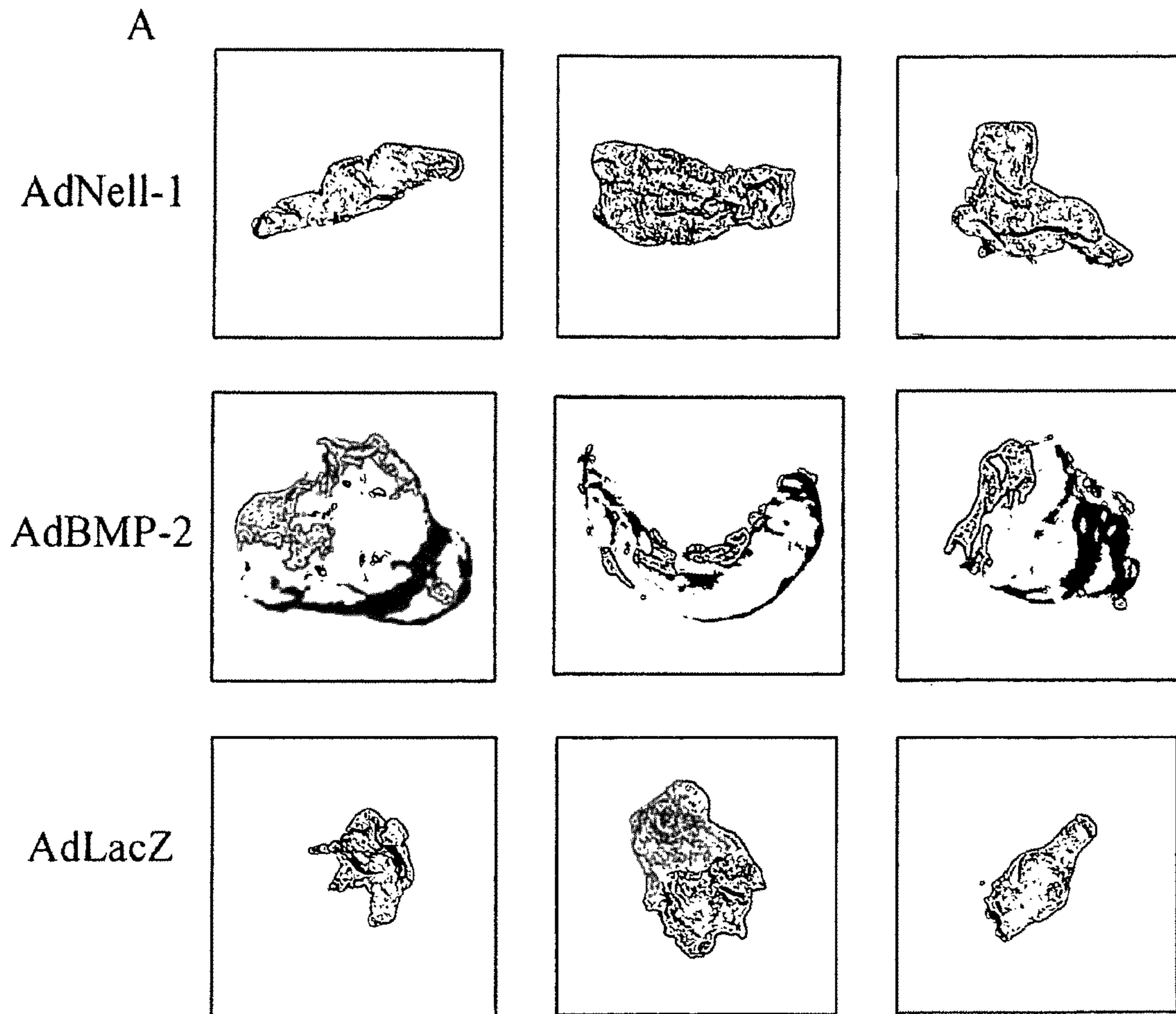


Figure 5A

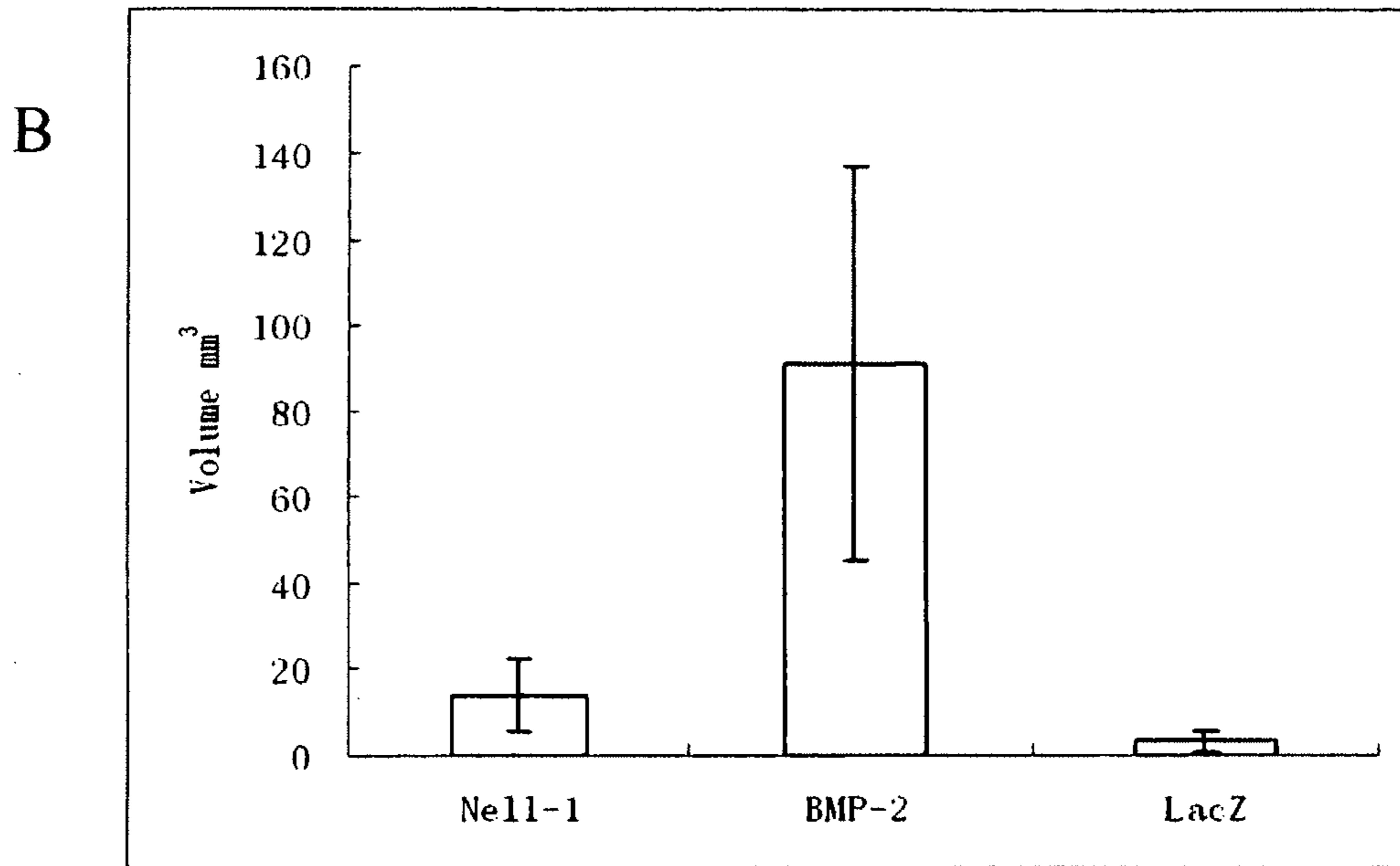


Figure 5B

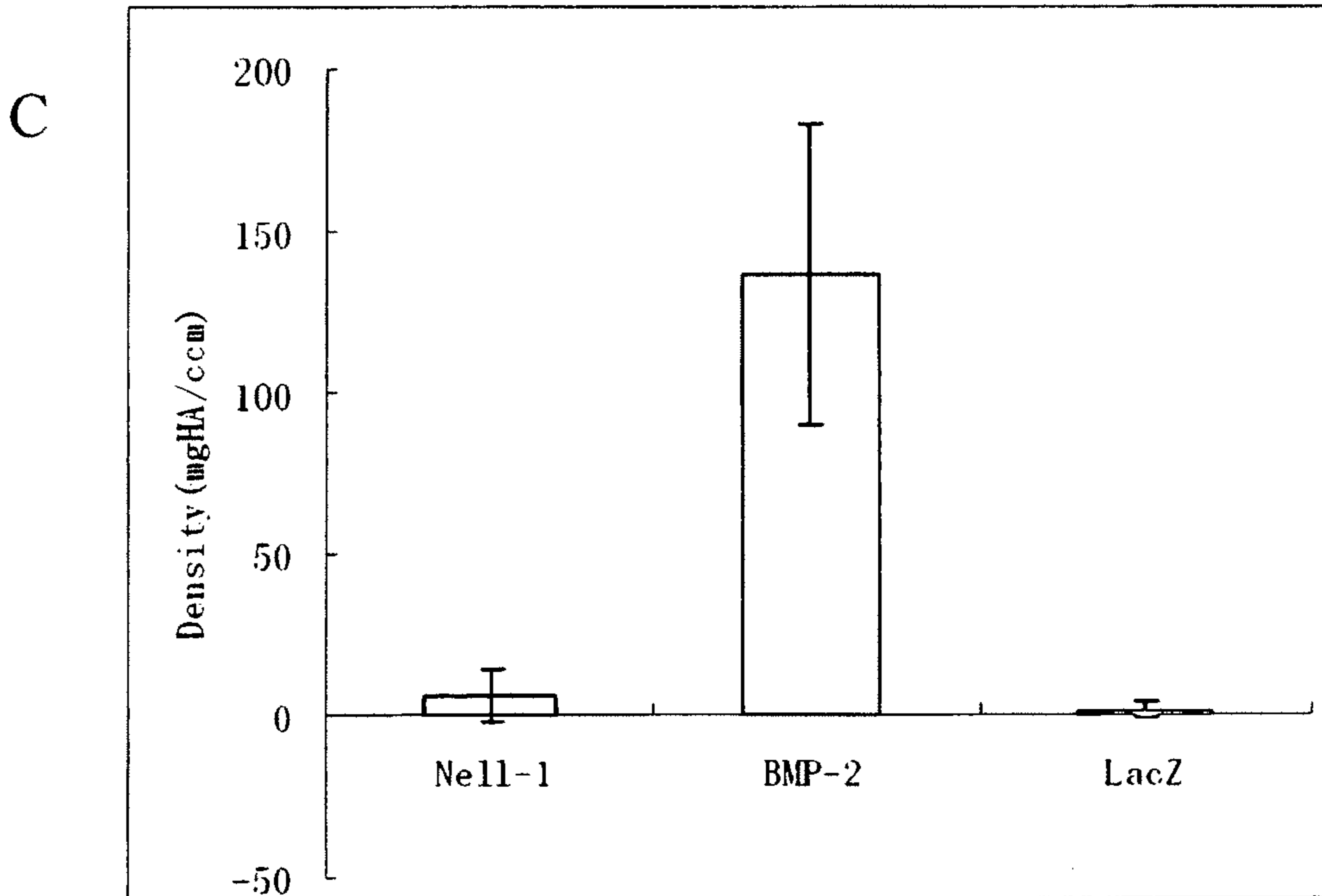


Figure 5C



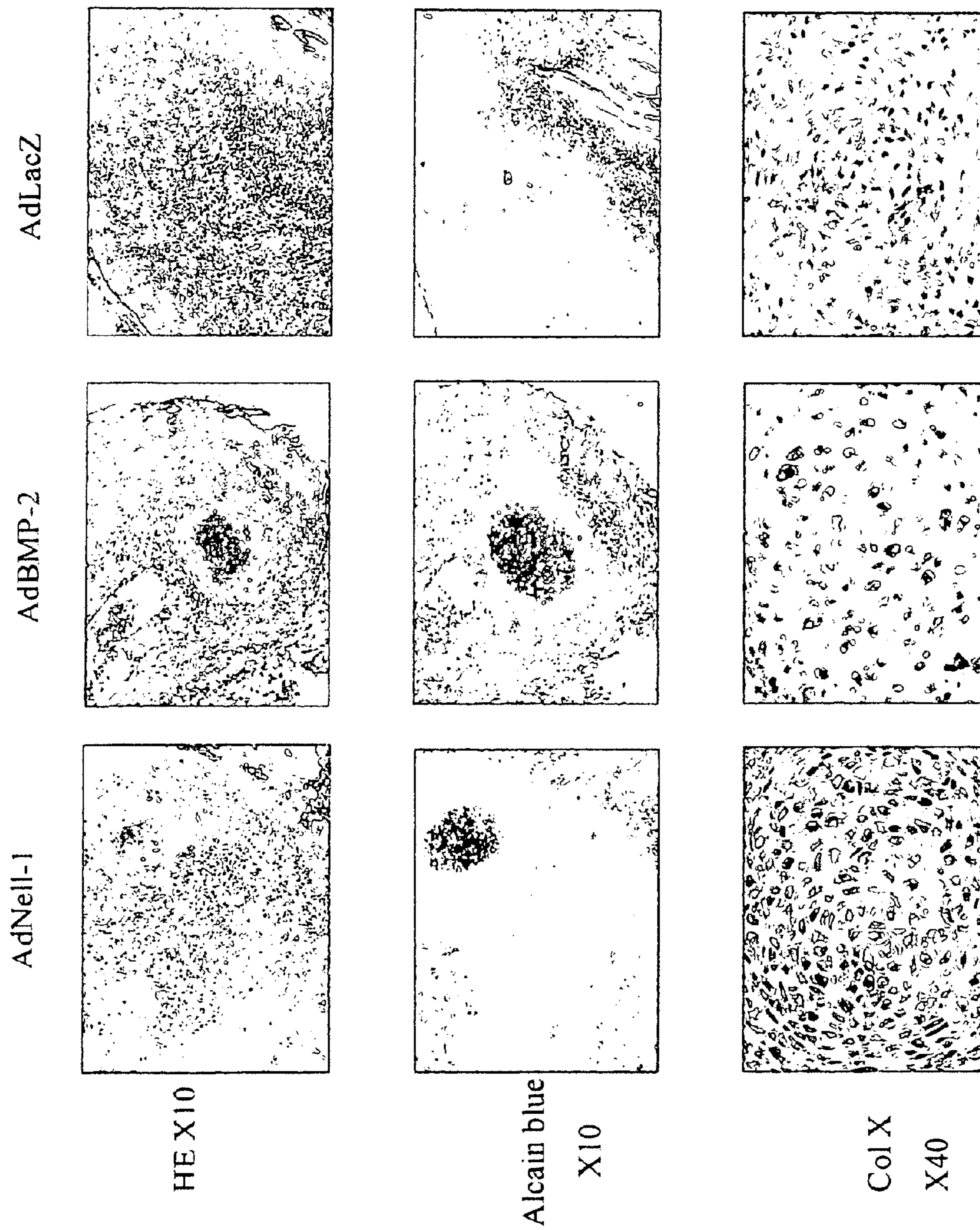


Figure 6

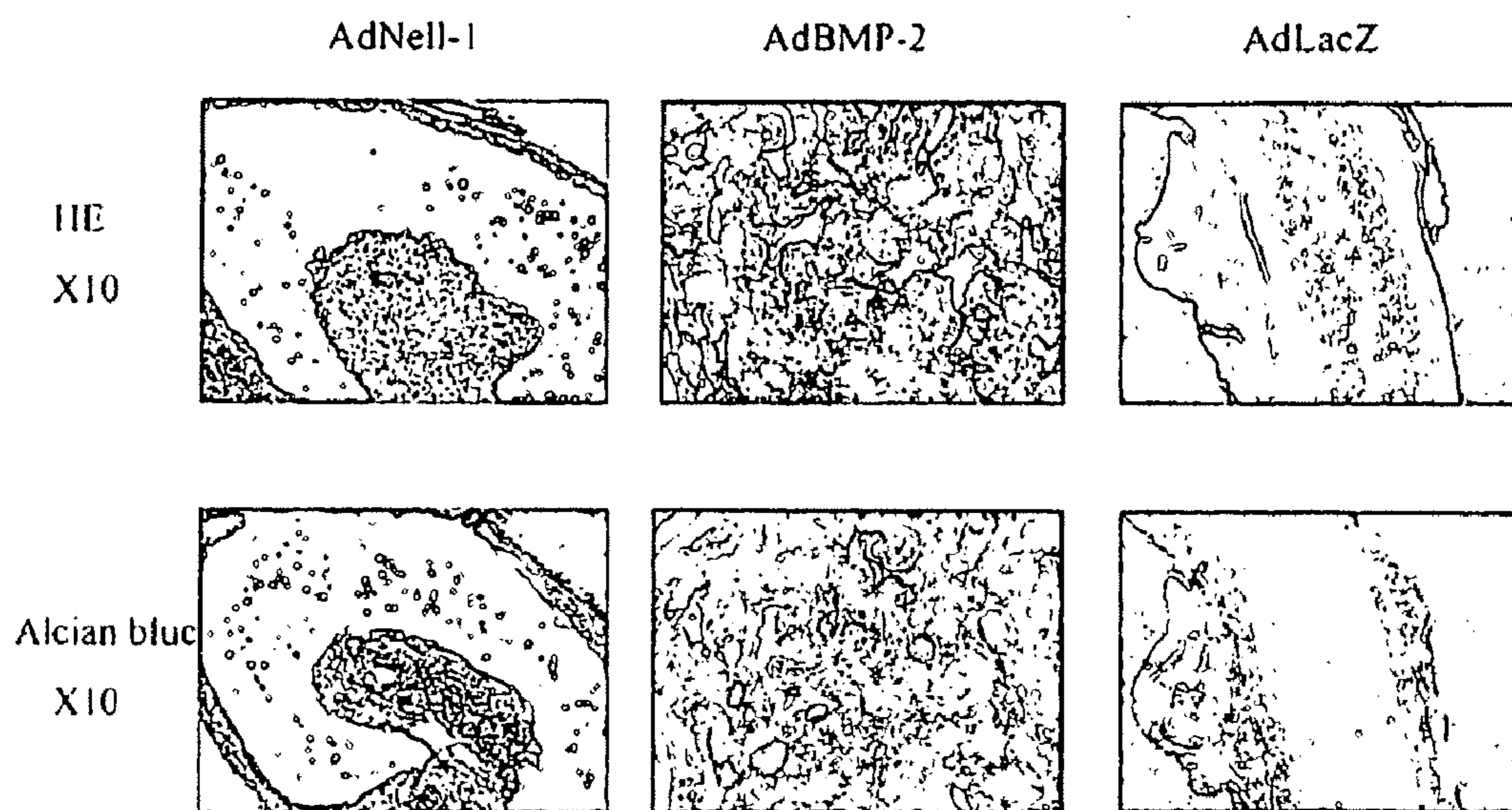


Figure 7

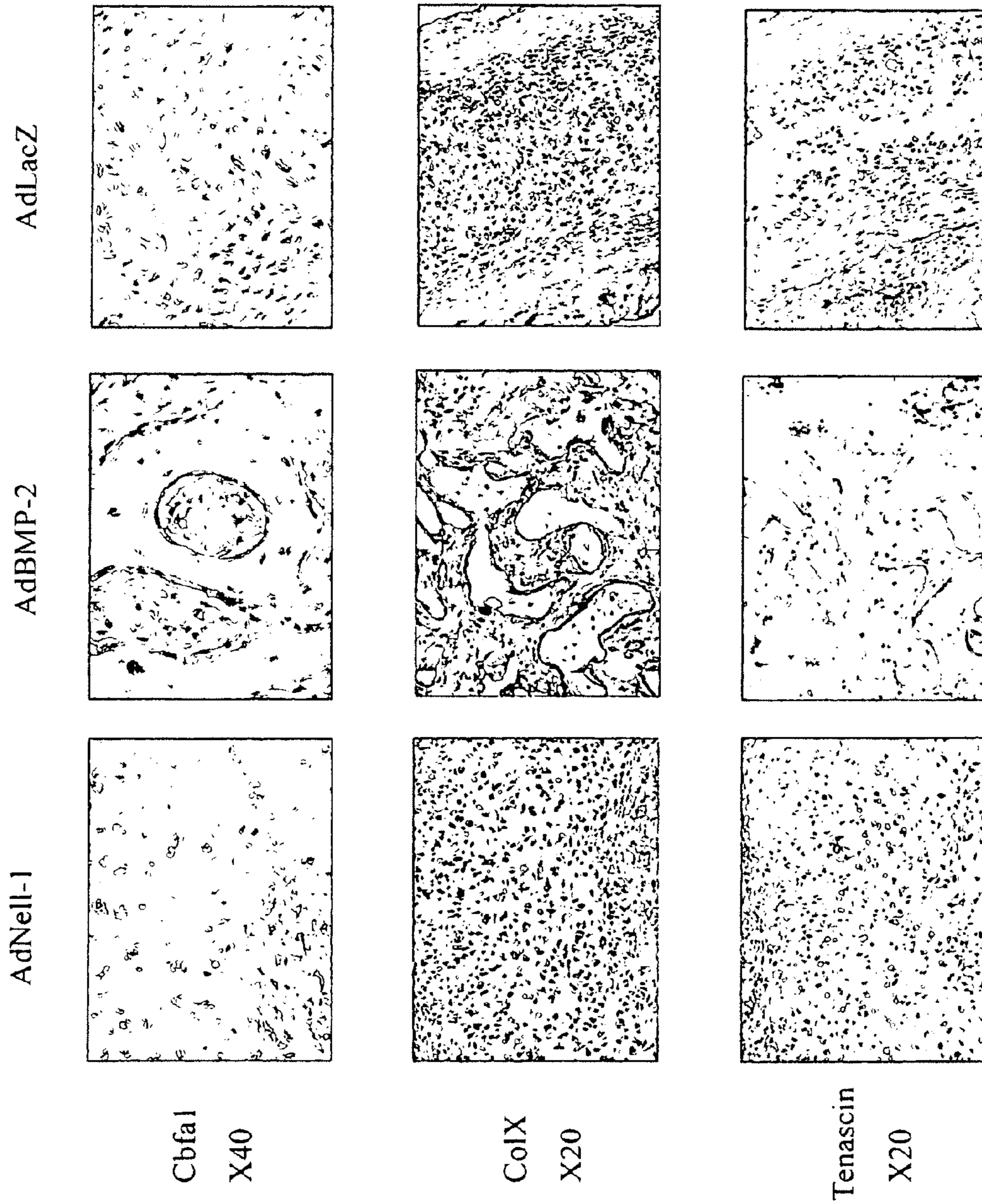


Figure 8

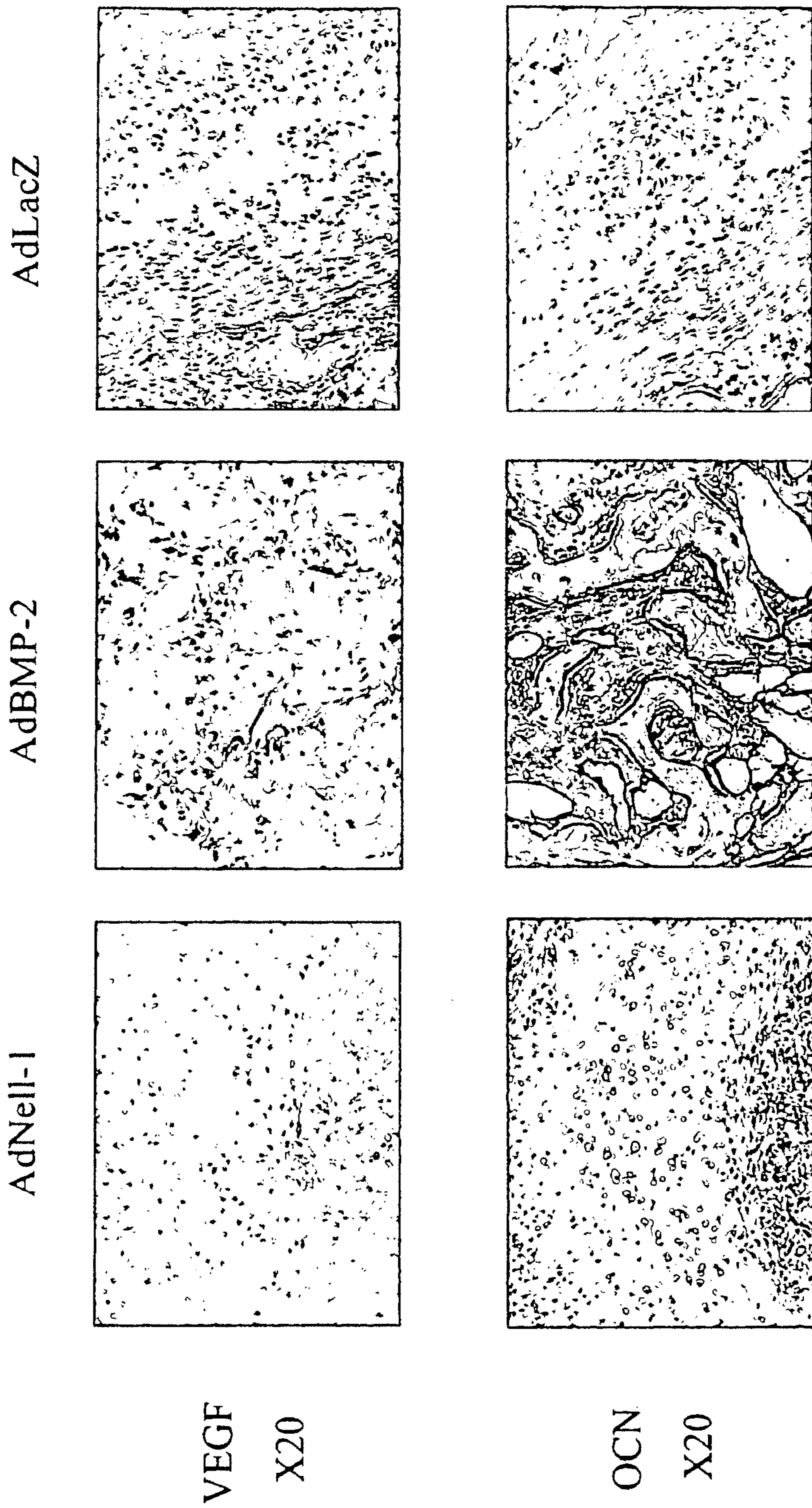
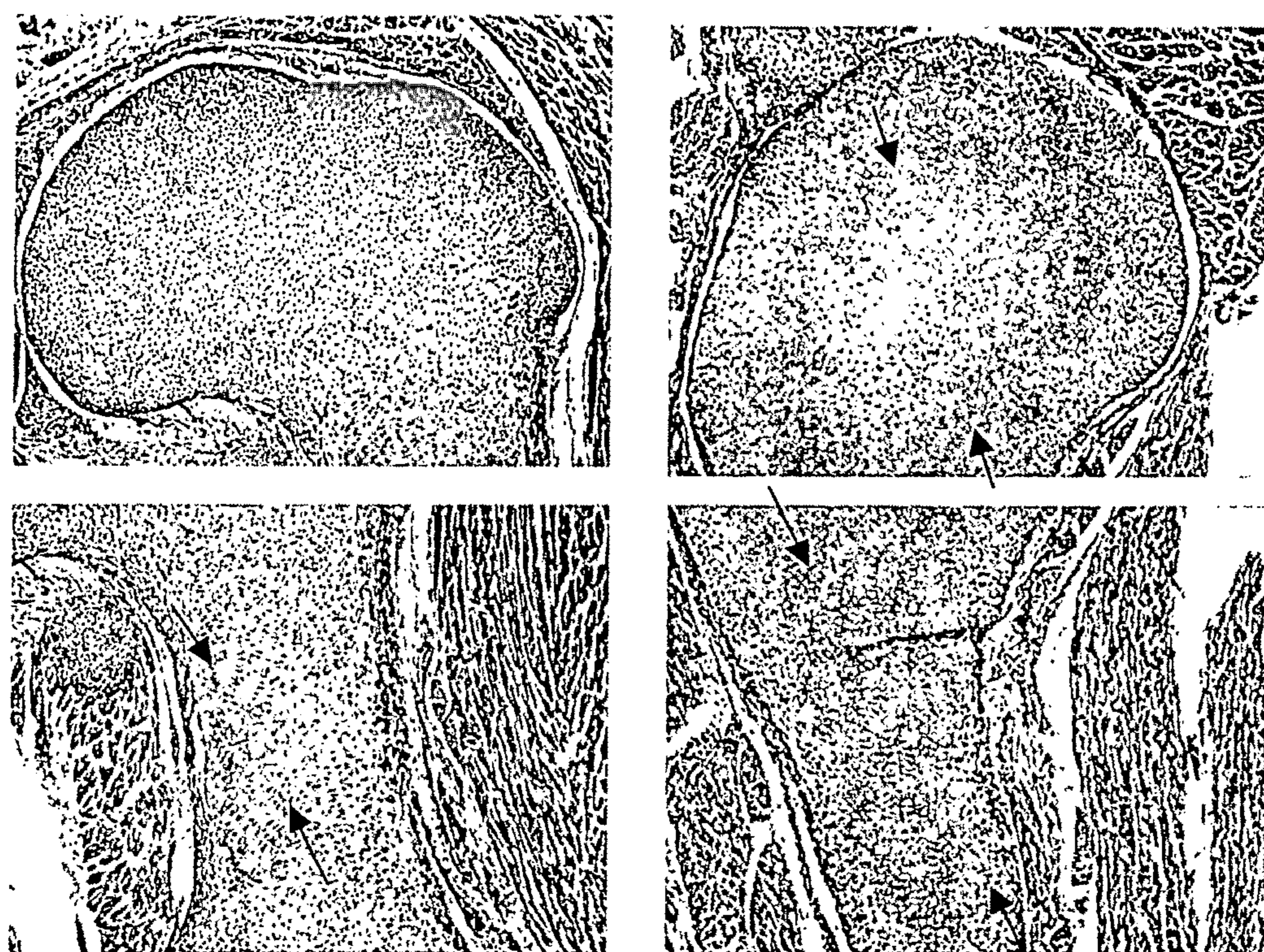


Figure 9



Control

Nell-1

Figure 10

**COMPOSITION FOR PROMOTING  
CARTILAGE FORMATION OR REPAIR  
COMPRISING A NELL GENE PRODUCT AND  
METHOD OF TREATING  
CARTILAGE-RELATED CONDITIONS USING  
SUCH COMPOSITION**

**CROSS-REFERENCE TO RELATED  
APPLICATIONS**

This application is a divisional application of U.S. application Ser. No. 11/594,510, filed Nov. 7, 2006, issued as U.S. Pat. No. 7,687,462, the teaching of which is incorporated herein by reference in its entirety.

U.S. application Ser. No. 11/594,510 is a continuation-in-part of U.S. application Ser. No. 10/527,786, filed on Sep. 28, 2005, which is a U.S. National Phase of international application No. PCT/US2003/29281, filed on Sep. 15, 2003, which claims priority to U.S. provisional application No. 60/410,846, filed on Sep. 13, 2002, the teachings of which are incorporated herein by reference in their entirety. U.S. application Ser. No. 10/527,786 is abandoned.

U.S. application Ser. No. 11/594,510 is also a continuation-in-part of U.S. application Ser. No. 10/544,553, filed on May 15, 2006, which is a U.S. National Phase of PCT application PCT/US2004/003808, filed on Feb. 9, 2004, which claims priority to U.S. provisional application No. 60/445,672, filed on Feb. 7, 2003, and PCT/US2003/29281, filed on Sep. 15, 2003, the teachings of which are incorporated herein by reference in their entirety. U.S. application Ser. No. 10/544,553 issued as U.S. Pat. No. 7,544,486.

U.S. application Ser. No. 11/594,510 is also a continuation-in-part of international application No. PCT/US2006/005473, filed on Feb. 16, 2006, which claims priority to U.S. Provisional Application No. 60/653,722 filed on Feb. 16, 2005, the teachings of which are incorporated herein by reference in their entirety.

U.S. application Ser. No. 11/594,510 is also a continuation-in-part of U.S. application Ser. No. 11/392,294, filed on Mar. 28, 2006, the teachings of which are incorporated herein by reference in their entirety. U.S. application Ser. No. 11/392,294 issued as U.S. Pat. No. 7,776,361.

The teachings of all the copending applications are incorporated herein by reference in their entirety.

**STATEMENT AS TO RIGHTS TO INVENTIONS  
MADE UNDER FEDERALLY SPONSORED  
RESEARCH AND DEVELOPMENT**

This invention was made with Government support under Grant Nos. DE000422, DE014649, DE016107, DE016781, DE094001, and RR000865 awarded by the National Institutes of Health. The Government of the United States of America has certain rights in this invention.

**FIELD OF THE INVENTION**

The invention generally relates to a composition for cartilage formation or regeneration.

**BACKGROUND OF THE INVENTION**

Growth factors are substances, such as peptides, which affect the growth and differentiation of defined populations of cells in vivo or in vitro.

Cartilage is a type of dense connective tissue. It is composed of chondrocytes which are dispersed in a firm gel-like

matrix. Cartilage is avascular (contains no blood vessels) and nutrients are diffused through the matrix. Cartilage is found in the joints, the rib cage, the ear, the nose, in the throat and between intervertebral disks. There are three main types of cartilage: hyaline (e.g., costal cartilages, the cartilages of the nose, trachea, and bronchi, and the articular cartilages of joints), elastic (e.g., external ear, external auditory meatus, part of the Eustachian tube, epiglottis, and in some of the laryngeal cartilages) and fibrocartilage [e.g. meniscus (e.g., wrist triangular fibrocartilage complex, knee meniscus), intervertebral discs, temporomandibular joint disc, the pubic symphysis, and in some tendons and ligaments at their attachment to bones. One of the main purposes of cartilage is to provide a framework upon which bone deposition could begin (i.e., during endochondral ossification). Another important purpose of cartilage is to provide smooth surfaces for the movement of articulating bones. For example, articular cartilage, most notably that which is found in the knee joint, is generally characterized by very low friction, high wear resistance, and poor regenerative qualities. It is responsible for much of the compressive resistance and load bearing qualities of the knee joint and, without it, walking is painful to impossible. Yet another important purpose of cartilage is to provide, firm, yet flexible support (e.g., nasal cartilage, spinal discs, tracheal cartilage, knee meniscus, bronchial cartilage). For instance, cartilage such as the meniscus plays a crucial role in joint stability, lubrication, and force transmission. Under a weight bearing load, the meniscus maintains the balanced position of the femur on the tibia and distributes the compressive forces by increasing the surface contact area, thereby decreasing the average stress two to three times. Additionally, the menisci interact with the joint fluid to produce a coefficient of friction that is five times as slick as ice on ice. In another example, the intervertebral disc has several important functions, including functioning as a spacer, as a shock absorber, and as a motion unit. The gelatinous central portion of the disc is called the nucleus pulposus. It is composed of 80-90% water. The solid portion of the nucleus is Type II collagen and non-aggregated proteoglycans. The outer ligamentous ring around the nucleus pulposus is called the annulus fibrosus, which hydraulically seals the nucleus, and allows intradiscal pressures to rise as the disc is loaded. The annulus has overlapping radial bands, not unlike the plies of a radial tire, and this allows torsional stresses to be distributed through the annulus under normal loading without rupture. The disc functions as a hydraulic cylinder. The annulus interacts with the nucleus. As the nucleus is pressurized, the annular fibers serve a containment function to prevent the nucleus from bulging or herniating.

Cartilage can be damaged by wear, injury or diseases. As we age, the water and protein content of the body's cartilage changes. This change results in weaker, more fragile and thin cartilage. Osteoarthritis is a common condition of cartilage failure that can lead to limited range of motion, bone damage and invariably, pain. Due to a combination of acute stress and chronic fatigue, osteoarthritis directly manifests itself in a wearing away of the articulating surface and, in extreme cases, bone can be exposed in the joint. In another example, loss of the protective stabilizing meniscus leads to increased joint laxity or abnormal motions that lead to joint instability. The excessive motion and narrowed contact area promotes early arthritic changes. At the cellular level, there is initially a loss of cells from the superficial layer of the articular cartilage followed by cartilage splitting, subsequent thinning and erosion occurs, and finally protrusion of the underlying raw bone. The earliest arthritic changes have been noted three weeks after loss of the entire meniscus. In yet another

example, because both the discs and the joints that stack the vertebrae (facet joints) are partly composed of cartilage, these areas are subject to wear and tear over time (degenerative changes). As the inner nucleus dehydrates, the disc space narrows, and redundant annular ligaments bulge. With progressive nuclear dehydration, the annular fibers can crack and tear. Loss of normal soft tissue tension may allow the spinal segment to sublux (e.g. partial dislocation of the joint), leading to osteophyte formation (bone spurs), foraminal narrowing, mechanical instability, and pain. If the annular fibers stretch or rupture, allowing the pressurized nuclear material to bulge or herniate and compress neural tissues, pain and weakness may result. This is the condition called a pinched nerve, slipped disc, or herniated disc. Radiculopathy refers to nerve irritation caused by damage to the disc between the vertebrae. Mechanical dysfunction may also cause disc degeneration and pain (e.g. degenerative disc disease). For example, the disc may be damaged as the result of some trauma that overloads the capacity of the disc to withstand increased forces passing through it, and inner or outer portions of the annular fibers may tear. These torn fibers may be the focus for inflammatory response when they are subjected to increased stress, and may cause pain directly, or through the compensatory protective spasm of the deep paraspinal muscles.

There are several different repair options available for cartilage damage or failure. Osteoarthritis is the second leading cause of disability in the elderly population in the United States. It is a degenerative disorder that generally starts off relatively mild and escalates with time and wear. For those patients experiencing mild to moderate symptoms, the disorder can be dealt with by several non-surgical treatments. The use of braces and drug therapies, such as anti-inflammatories (ex. diclofenac, ibuprofen, and naproxen), COX-2 selective inhibitors, hydrocortisone, glucosamine, and chondroitin sulfate, have been shown to alleviate the pain caused by cartilage deficiency and some claim they can slow the degenerative process.

Most surgical treatments for articular cartilage, short of total joint replacement, can be divided into various treatment groups. Treatments that remove the diseased and undermined cartilage with an aim to stop inflammation and pain include shaving (chondrectomy) and debridement. Another group of treatments consists of a range of abrasive procedures aimed at triggering cartilage production, such as drilling, microfracture surgery, chondroplasty, and spongialization. Abrasion, drilling, and microfracture originated 20 years ago. They rely on the phenomenon of spontaneous repair of the cartilage tissue following vascular injury to the subchondral plate of the bone. Laser assisted treatments, currently experimental, compose another category; they combine the removal of diseased cartilage with cartilage reshaping and also induce cartilage proliferation. Additional treatments include autologous cartilage implants (e.g., Carticel by Genzyme). Other treatments, more applicable to meniscal cartilage, include early surgical intervention and suture repair of torn structures or allograft meniscus transplantation in severe injury cases.

Although the overwhelming majority of patients with a herniated disc and sciatica heal without surgery, if surgery is indicated procedures include removal of the herniated disc with laminotomy (producing a small hole in the bone of the spine surrounding the spinal cord), laminectomy (removal of the bony wall adjacent to the nerve tissues), by needle technique through the skin (percutaneous discectomy), disc-dissolving procedures (chemonucleolysis), and others. For patients with mechanical pain syndrome, unresponsive to conservative treatment, and disabling to the individual's way

of life, the problem can be addressed by spinal fusion, intradiscal electrothermal coagulation (or annuloplasty), posterior dynamic stabilization, artificial disc technologies, or still experimental disc regeneration therapies using various molecular based therapies delivered using proteins, peptides, gene therapies, or nucleotides. Although numerous methods have been described for treatment of cartilage problems, it is clear that many are artificial or mechanically based solutions that do not seek to recreate normal cartilage tissue biology. Therefore, there is a need for methods for stimulating cartilage formation.

The embodiments described below address the above identified issues and needs.

#### SUMMARY OF THE INVENTION

The present invention is related to agents and methods for inducing cartilage formation or repair using a NELL peptide or related agent (collectively referred as "agent"). The composition can include a NELL peptide, a Nell-like molecule, and optionally at least one other active agent, cells, and biocompatible material implanted for the purpose of cartilage repair (i.e., hyaline cartilage, elastic cartilage, or fibrocartilage).

In some embodiments, the present invention provides a composition that contains an effective amount of at least one agent for either directly or indirectly promoting the generation of cartilage for treating, preventing or ameliorating a cartilage related medical condition. One of the agents for direct promotion of cartilage generation can be NELL peptides or NELL-based gene therapy or NELL-gene product enhancers applied to chondrogenic cells such as, but not limited to, chondroblasts, chondrocytes, or chondroprogenitor cells, adult and embryonic stem cells, bone marrow cells, bone marrow stromal cells, mesenchymal cells, a fibroblast, or adipose derived cells. The agent for indirect promotion of cartilage generation (e.g., through inducing chondroblast/chondrocyte differentiation) can be, e.g., one of NELL peptide, or agonists of NELL peptide receptors.

In some embodiments, the composition can include, e.g., one or more inhibitors or antagonists of NELL peptide receptors, high dose NELL peptides, or combinations thereof. Such a composition is effective for inhibition of chondrogenic differentiation by inhibiting potential or committed chondrogenic cells such as, but not limited to, osteoblasts, osteoprogenitor cells, stem cells, bone marrow cells, fibroblastic cells, dural cells, periosteal cells, pericytes, and/or muscle cells.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows increased cartilage maturation and hypertrophy in femoral head cartilage of NELL1 overexpression mice compared with wild type littermate. On the left is wild type newborn femoral head cartilage demonstrating small, less mature chondrocytes in the femoral head. On the right is the NELL1 over-expression transgenic mice demonstrating well differentiated, more mature, hypertrophic chondrocytes present throughout the femoral head with large nuclei and vacuoles present.

FIGS. 2A-2F show increased meniscus development in E18 NELL1 overexpression mice compared with wild type littermate. FIGS. 2A and 2B with arrows pointing at the meniscus between the femoral and tibial cartilage head in wild type (FIG. 2A) and NELL1 overexpression (FIG. 2B) animals. FIGS. 2C and 2D are higher magnification views of FIGS. 2A and 2B. FIG. 2E is a higher magnification of the wild type control shown in 2C demonstrating less differenti-

## 5

ated chondrocytes with minimal hypertrophy. FIG. 2F is a higher magnification of the NELL1 overexpression animal shown in 2D demonstrating significantly more differentiated chondrocyte in the cartilage matrix. Vacuoles in the hypertrophic chondrocytes are observed indicating well differentiation of chondrocyte in the meniscus.

FIGS. 3A and 3B show adenovirus transduction of goat primary chondrocytes isolated from auricular cartilage. FIG. 3A shows the efficiency of adenoviral (Ad) transduction with significant number of positively stained cells expressing beta-galactosidase. FIG. 3B is a Western gel demonstrating significant NELL1 protein expression in the AdNELL1 transduced goat chondrocytes (relative to beta-actin controls) and no NELL1 protein expression in Ad BMP2 or AdLacZ (control) transduced goat chondrocytes.

FIGS. 4A and 4B show gross appearance of AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. NELL1 transduced samples were significantly larger than control by both inspection (FIG. 4A) and weight (FIG. 4B). In addition, NELL1 transduced samples did not demonstrate the discoloration present in the BMP2 transduced samples.

FIGS. 5A-C show micro computed tomography (CT) examination of the samples shown in FIG. 4. FIG. 5A demonstrates undesirable mineralization (red coloring) in the AdBMP2 transduced specimens but not AdNELL1 or AdLacZ specimens. FIG. 5B demonstrates that NELL1 induces significantly more cartilage mass than AdLacZ controls. FIG. 5C demonstrates that AdBMP2 significantly increased density (another indicator of mineralization) in the specimens.

FIG. 6 shows histologic appearance of AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 2 weeks after implantation/injection into nude mice. Hematoxylin and eosin (H&E) staining (1<sup>st</sup> row) shows evidence of increased cartilage formation in the AdNELL1 and AdBMP2 transduced specimens relative to AdLacZ controls. Alcian blue staining which stains cartilage (2<sup>nd</sup> row) also demonstrates increased cartilage formation in the AdNELL1 and AdBMP2 transduced specimens relative to AdLacZ controls. Type X collagen (ColX) immunostaining which stains more mature cartilage cells (3<sup>rd</sup> row) demonstrates increased staining in the AdNELL1 and AdBMP2 transduced specimens.

FIG. 7 shows histologic appearance of AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. H&E staining (1<sup>st</sup> row) shows significant cartilage formation in the AdNELL transduced samples with no evidence of bone formation, while AdBMP2 samples show significant bone formation. A small amount of cartilage formation is seen the AdLacZ controls. Alcian blue staining (2<sup>nd</sup> row) also demonstrates significant cartilage formation in the AdNELL transduced samples with no evidence of bone formation, while AdBMP2 samples show significant bone formation and minimal cartilage formation. A small amount of immature cartilage formation is seen the AdLacZ controls.

FIG. 8 shows immunostaining for bone marker Cbfa1/Runx2 and cartilage markers ColX and tenascin in AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. Tenascin is intimately associated with the development of articular cartilage and other permanent cartilages whereas absence or reduced amounts of this matrix protein characterize transient cartilages which undergo maturation and are replaced by bone (Pacifici, M., M. Iwamoto, et

## 6

al. Tenascin is associated with articular cartilage development. *Dev Dyn* 198(2): 123-34, 1993). Cbfa1/Runx2 is minimally expressed in cartilaginous AdNELL1 or control AdLacZ transduced samples and moderately expressed in bony AdBMP2 transduced samples (1<sup>st</sup> row). ColX is highly expressed and localized largely to cells in cartilaginous AdNELL1 samples without evidence of bone formation, while ColX is largely associated with the extracellular matrix rather than cells in the AdBMP2 treated samples (2<sup>nd</sup> row). Tenascin is highly expressed in AdNELL1 samples and minimally present in AdBMP2 and control AdLacZ samples (3<sup>rd</sup> row).

FIG. 9 shows immunostaining for endochondral ossification associated angiogenic growth factor, vascular endothelial growth factor (VEGF), and bone marker osteocalcin (OCN) in AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. Both VEGF and OCN are not expressed in cartilaginous AdNELL1 or control AdLacZ transduced samples and moderately expressed in bony AdBMP2 transduced samples.

FIG. 10 shows the histology of long bone cartilage in NELL-1 over expression mice. NELL1 is expressed throughout the tibia during endochondral bone formation including both articular cartilage region (Upper panel) and also the long bone formation region (lower panel). Upper panel demonstrates that NELL1 can modulate and increase cartilage differentiation in the articular cartilage region. Accordingly, these data show that increased NELL peptide activity directly (e.g., through addition of NELL peptides or increased NELL peptide expression) or indirectly (e.g., through addition of NELL peptide enhancers and/or NELL peptide receptor agonists and/or activators) promotes cartilage formation. In the lower panel, in the long bone shaft region where bone formation originated, increased NELL1 causes cartilage formation and then hypertrophy and increased bone formation through endochondral ossification.

## DETAILED DESCRIPTION

The present invention is related to agents and methods for inducing cartilage formation or repair using a NELL peptide or related agent (collectively referred as "agent"). The composition can include a NELL peptide, a Nell-like molecule, and optionally at least one other active agent, cells, and biocompatible material implanted for the purpose of articular cartilage repair.

In some embodiments, the present invention provides a composition that contains an effective amount of at least one agent for either directly or indirectly promoting the generation of cartilage for treating, preventing or ameliorating a cartilage related medical condition. One of the agents for direct promotion of cartilage generation can be NELL peptides applied to chondrogenic cells such as, but not limited to, chondroblasts, chondrocytes, or chondroprogenitor cells, stem cells, bone marrow cells, a bone marrow stromal cells, a fibroblast, or adipose derived cells. The agent for indirect promotion of cartilage generation (e.g., through inducing chondroblast/chondrocyte differentiation) can be, e.g., one of NELL peptide, or agonists of NELL peptide receptors.

In some embodiments, the present invention includes a systemic or local application of the composition described herein to a mammalian subject (e.g., a human being) to promote cartilage formation or regeneration.

In some embodiments, the composition can include, e.g., one or more inhibitors or antagonists of NELL peptide receptors, high dose NELL peptides, or combinations thereof. Such



a composition is effective for inhibition of chondrogenic differentiation by inhibiting potential or committed chondrogenic cells such as, but not limited to, osteoblasts, osteoprogenitor cells, stem cells, bone marrow cells, fibroblastic cells, dural cells, periosteal cells, pericytes, and/or muscle cells.

The effectiveness of the present invention for cartilage formation or regeneration are shown in FIGS. 1-10.

FIG. 1 shows increased cartilage maturation and hypertrophy in femoral head cartilage of NELL1 overexpression mice compared with wild type littermate. On the left is wild type newborn femoral head cartilage demonstrating small, less mature chondrocytes in the femoral head. On the right is the NELL1 over-expression transgenic mice demonstrating well differentiated, more mature, hypertrophic chondrocytes present throughout the femoral head with large nuclei and vacuoles present. Note the absence of mineralization in the hypertrophied cartilage. These studies demonstrate that NELL1 increases chondrocyte maturation, hypertrophy without necessarily inducing mineralization.

FIGS. 2A-2F show increased meniscus development in E18 NELL1 overexpression mice compared with wild type littermate. FIGS. 2A and 2B with arrows pointing at the meniscus between the femoral and tibial cartilage head in wild type (FIG. 2A) and NELL1 overexpression (FIG. 2B) animals. FIGS. 2C and 2D are higher magnification views of FIGS. 2A and 2B. FIG. 2E is a higher magnification of the wild type control shown in 2C demonstrating less differentiated chondrocytes with minimal hypertrophy. FIG. 2F is a higher magnification of the NELL1 overexpression animal shown in 2D demonstrating significantly more differentiated chondrocyte in the cartilage matrix. Vacuoles in the hypertrophic chondrocytes are observed indicating well differentiation of chondrocyte in the meniscus. This data indicates that Nell-1 can promote meniscus formation and differentiation.

FIGS. 3A and 3B show adenovirus transduction of goat primary chondrocytes isolated from auricular cartilage. FIG. 3A shows the efficiency of adenoviral (Ad) transduction with significant number of positively stained cells expressing beta-galactosidase. FIG. 3B is a Western gel demonstrating significant NELL1 protein expression in the AdNELL1 transduced goat chondrocytes (relative to beta-actin controls) and no NELL1 protein expression in Ad BMP2 or AdLacZ (control) transduced goat chondrocytes. These studies demonstrate that there is efficient adenoviral transduction and that AdNELL1, but not AdBMP2, increases NELL1 protein expression.

FIGS. 4A and 4B show gross appearance of AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. NELL1 transduced samples were significantly larger than control by both inspection (FIG. 4A) and weight (FIG. 4B). In addition, NELL1 transduced samples did not demonstrate the discoloration present in the BMP2 transduced samples. These studies unexpectedly demonstrate that although BMP2 induces a larger tissue mass, the appearance of the induced mass is not consistent with a purely cartilaginous phenotype.

FIGS. 5A-C show micro computed tomography (CT) examination of the samples shown in FIG. 4. FIG. 5A demonstrates undesirable mineralization (red coloring) in the AdBMP2 transduced specimens but not AdNELL1 or AdLacZ specimens. FIG. 5B demonstrates that NELL1 induces significantly more cartilage mass than AdLacZ controls. FIG. 5C demonstrates that AdBMP2 significantly increased density (another indicator of mineralization) in the specimens. These studies quantitatively demonstrate that

although BMP2 induces a larger tissue mass, the induced mass is largely mineralized and is not consistent with a purely cartilaginous phenotype.

FIG. 6 shows histologic appearance of AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 2 weeks after implantation/injection into nude mice. Hematoxylin and eosin (H&E) staining (1<sup>st</sup> row) shows evidence of increased cartilage formation in the AdNELL1 and AdBMP2 transduced specimens relative to AdLacZ controls. Alcian blue staining which stains cartilage (2<sup>nd</sup> row) also demonstrates increased cartilage formation in the AdNELL1 and AdBMP2 transduced specimens relative to AdLacZ controls. Type X collagen (ColX) immunostaining which stains more mature cartilage cells (3<sup>rd</sup> row) demonstrates increased staining in the AdNELL1 and AdBMP2 transduced specimens. Collectively, these data indicate that both AdNELL1 and AdBMP2 induce comparable cartilage formation and maturation at 2 weeks.

FIG. 7 shows histologic appearance of AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. H&E staining (1<sup>st</sup> row) shows significant cartilage formation in the AdNELL transduced samples with no evidence of bone formation, while AdBMP2 samples show significant bone formation. A small amount of cartilage formation is seen the AdLacZ controls. Alcian blue staining (2<sup>nd</sup> row) also demonstrates significant cartilage formation in the AdNELL transduced samples with no evidence of bone formation, while AdBMP2 samples show significant bone formation and minimal cartilage formation. A small amount of immature cartilage formation is seen the AdLacZ controls. Collectively, these data indicate that by 4 weeks, AdNELL1 can continue to induce and maintain a cartilaginous phenotype, while AdBMP2 goes on to form bone and is unable to maintain a cartilaginous phenotype in chondrogenic cells.

FIG. 8 shows immunostaining for bone marker Cbfa1/Runx2 and cartilage markers ColX and tenascin in AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. Tenascin is intimately associated with the development of articular cartilage and other permanent cartilages whereas absence or reduced amounts of this matrix protein characterize transient cartilages which undergo maturation and are replaced by bone (Pacifci, M., M. Iwamoto, et al. Tenascin is associated with articular cartilage development. *Dev Dyn* 198(2): 123-34, 1993). Cbfa1/Runx2 is minimally expressed in cartilaginous AdNELL1 or control AdLacZ transduced samples and moderately expressed in bony AdBMP2 transduced samples (1<sup>st</sup> row). ColX is highly expressed and localized largely to cells in cartilaginous AdNELL1 samples without evidence of bone formation, while ColX is largely associated with the extracellular matrix rather than cells in the AdBMP2 treated samples (2<sup>nd</sup> row). Tenascin is highly expressed in AdNELL1 samples and minimally present in AdBMP2 and control AdLacZ samples (3<sup>rd</sup> row). These studies show NELL1 is able to induce molecules (e.g., tenascin) associated with development of articular cartilage and other permanent cartilages.

FIG. 9 shows immunostaining for endochondral ossification associated angiogenic growth factor, vascular endothelial growth factor (VEGF), and bone marker osteocalcin (OCN) in AdNELL1, AdBMP2, or AdLacZ (control) transduced goat primary chondrocytes 4 weeks after implantation/injection into nude mice. Both VEGF and OCN are not expressed in cartilaginous AdNELL1 or control AdLacZ transduced samples and moderately expressed in bony AdBMP2 transduced samples. These data show that NELL1

does not promote angiogenesis and that NELL1 may inhibit angiogenesis in cartilaginous samples.

FIG. 10 shows the histology of long bone cartilage in NELL-1 over expression mice. NELL1 is expressed throughout the tibia during endochondral bone formation including both articular cartilage region (Upper panel) and also the long bone formation region (lower panel). Upper panel demonstrates that NELL1 can modulate and increase cartilage differentiation in the articular cartilage region. Accordingly, these data show that increased NELL peptide activity directly (e.g., through addition of NELL peptides or increased NELL peptide expression) or indirectly (e.g., through addition of NELL peptide enhancers and/or NELL peptide receptor agonists and/or activators) promotes cartilage formation. In the lower panel, in the long bone shaft region where bone formation originated, increased NELL1 causes cartilage formation and then hypertrophy and increased bone formation through endochondral ossification. Accordingly, these data show that increased NELL peptide activity directly or indirectly promotes cartilage formation, cartilage hypertrophy and endochondral ossification. The absence of NELL1 associates with less differentiated articular chondroblast/chondrocyte phenotype and less hypertrophy which is important to prevent articular cartilage replaced by bone. Accordingly, the inhibition of NELL peptide activity directly (through decreased NELL peptide expression or use of NELL peptide inhibitors) or indirectly (through NELL peptide receptor antagonists and/or inhibitors) can prevent cartilage hypertrophy and endochondral ossification and promote maintenance of a less differentiated or hypertrophied cartilage phenotype. Overall, these data are not intended to be limiting, but rather to show that NELL has broad effects on osteochondroprogenitor cell types and that the exact phenotype induced by NELL depends on a complex interplay between the amount and timing of NELL application, the exact cell type, cell differentiation state, and the microenvironment.

#### DEFINITIONS

The term “cartilage” is understood to encompass hyaline, elastic and fibrocartilage and can refer to any cartilaginous component of a mammal. For instance, spinal disc and knee meniscus are fibrocartilaginous structures that are included in the definition of cartilage.

The terms “polypeptide”, “peptide” and “protein” can be used interchangeably herein to refer to a polymer of amino acid residues. The terms can apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

The term “NELL” refers to “NELL1 and NELL2 peptide. A NELL1 peptide is a protein which can be expressed by the NELL1 gene or cDNA and includes SEQ ID NO: 2, 4, and 6. The NELL1 peptide can include a NELL1 peptide fragment that retains the ability to induce chondrogenic cell differentiation for cartilage formation. A NELL2 peptide is a protein which can be expressed by the NELL2 gene or cDNA and includes SEQ ID NO: 8, 10, 12 and 14. The NELL2 peptide can include NELL2 peptide fragments that retain similar activity to the full NELL2 peptide sequence. Nell-1, Nell-2, etc. intact proteins, completely or partially glycosylated, fragments, deletions, additions, amino acid substitutes, mutations and modifications that retain the biological characteristics of the naturally occurring agents. Small molecules containing Nell active domains and Nell binding sites.

In some embodiments, the term “NELL peptide” can include a fragment of a NELL1 or NELL2 related polypeptide.

In some embodiments, the term “NELL peptide” can include a NELL related agent. For example, a NELL peptide related agent can include any polypeptide with significant homology to a NELL peptide or a fragment thereof. Significant homology can be a homology of higher than about 50% homology to a NELL peptide, e.g., higher than about 60% homology to a NELL peptide, higher than about 70% homology to a NELL peptide, or higher than about 80% homology to a NELL peptide.

The NELL peptides can be natural and/or recombinant NELL peptides with a non-mutated wild-type sequence or recombinant NELL peptides with a mutated wild-type sequence that still contains significant homology to NELL peptides. In addition, NELL peptides can be derived from, but not limited to, an organism such as human cells, bacteria, yeast, or insect or plant cells. In some embodiments, the term “NELL peptide” includes structural, functional or conformational equivalents of NELL peptide. As used herein, a structural equivalent of a NELL peptide refers to a protein or peptide including a structure equivalent or substantially similar to that of a NELL peptide or of a functional domain of a NELL peptide. A functional equivalent of a NELL peptide refers to a protein or peptide having a function equivalent or substantially similar to that of a NELL peptide or of a functional domain of a NELL peptide. A conformational equivalent of a NELL peptide refers to a protein or peptide having a conformation equivalent or substantially similar to that of a NELL peptide or of a functional domain of a NELL peptide.

In some embodiments, the NELL peptide described herein can be a derivative of the NELL peptide. The term “derivative” as used herein, refers to any chemical or biological compounds or materials derived from a NELL peptide, structural equivalents thereof, or conformational equivalents thereof. For example, such a derivative can include any pro-drug form, PEGylated form, or any other form of a NELL peptide that renders the NELL peptide more stable or to have a better osteophilicity or lipophilicity. In some embodiments, the derivative can be a NELL peptide attached to poly(ethylene glycol), a poly(amino acid), a hydrocarbyl short chain having C1-C20 carbons, or a biocompatible polymer. In some embodiments, the term “derivative” can include a NELL peptide mimetics. Synthesis of mimetics of a peptide is well document in the art. The following describes an example of the basic procedure for the synthesis of a peptide, including a peptide mimetics:

Before the peptide synthesis starts, the amine terminus of the amino acid (starting material) can protected with Fmoc (9-fluoromethyl carbamate) or other protective groups, and a solid support such as a Merrifield resin (free amines) is used as an initiator. Then, step (1) through step (3) reactions are performed and repeated until the desired peptide is obtained: (1) a free-amine is reacted with carboxyl terminus using carbodiimide chemistry, (2) the amino acid sequence is purified, and (3) the protecting group, e.g., the Fmoc protecting group, is removed under mildly acidic conditions to yield a free amine. The peptide can then be cleaved from the resin to yield a free standing peptide or peptide mimetics.

In some embodiments, the peptide derivative described herein includes a physically or chemically modified NELL peptide. Physically modified peptide can be modification by, for example, modification by ionic force such as forming an ionic pair with a counterion, modification by hydrogen bonding, modification by modulation of pH, modulation by solvent selection, or modification by using different protein fold-

ing/unfolding procedures, which can involve selection of folding/unfolding temperature, pH, solvent, and duration at different stage of folding/unfolding.

In some embodiments, the peptide derivative can include a chemically modified NELL peptide. For example, a short hydrocarbon group(s) (e.g. methyl or ethyl) can be selectively attached to one or multiple sites on the NELL peptide molecule to modify the chemical and/or physical properties of the peptide. In some embodiments, a mono-, oligo- or poly(ethylene glycol) (PEG) group(s) can be selectively attached to one or multiple sites on the NELL peptide molecule to modify the chemical and/or physical properties of the peptide by commonly known protein PEGylation procedures (see, e.g., Mok, H., et al., *Mol. Ther.*, 11(1):66-79 (2005)).

The terms "NELL1 cDNA" can refer to SEQ ID NO:1, 3 and 5, and "NELL2 cDNA" can refer to SEQ ID NO:7, 9, 11 and 13.

The term "antibody" refers to any antibody that specifically binds to a NELL peptide or a related agent. The term can include various forms of modified or altered antibodies, such as an intact immunoglobulin, an Fv fragment containing only the light and heavy chain variable regions, an Fv fragment linked by a disulfide bond, a Fab or (Fab)<sup>2</sup> fragment containing the variable regions and parts of the constant regions, a single-chain antibody and the like. An antibody can include intact molecules as well as fragments thereof, such as, Fab and F(ab')<sup>2</sup>, and/or single-chain antibodies (e.g. scFv) which can bind an epitopic determinant. An antibody can be of animal (such as mouse or rat) or human origin or can be chimeric or humanized. Antibodies can be polyclonal or monoclonal antibodies ("mAb's"), such as monoclonal antibodies with specificity for a polypeptide encoded by a NELL1 or NELL 2 protein.

The term "capture agent" can refer to molecules that specifically bind other molecules to form a binding complex such as antibody-antigen, lectin-carbohydrate, nucleic acid-nucleic acid, biotin-avidin, and the like.

The term "specifically binds" can refer to a biomolecule (e.g., protein, nucleic acid, antibody, etc.), refers to a binding reaction which is determinative of the presence biomolecule in heterogeneous population of molecules (e.g., proteins and other biologics). Thus, under designated conditions (e.g. immunoassay conditions in the case of an antibody or stringent hybridization conditions in the case of a nucleic acid), the specified ligand or antibody can bind to its particular "target" molecule and can not bind in a significant amount to other molecules present in the sample.

The terms "nucleic acid" or "oligonucleotide" can refer to at least two nucleotides covalently linked together. A nucleic acid of the present invention can be single-stranded or double stranded and can contain phosphodiester bonds, although in some cases, nucleic acid analogs can be included that can have alternate backbones, comprising, for example, phosphoramidate, phosphorothioate, phosphorodithioate, omethylphosphoramidite linkages, and/or peptide nucleic acid backbones and linkages. Analog nucleic acids can have positive backbones and/or non-ribose backbones. Nucleic acids can also include one or more carbocyclic sugars. Modifications of the ribose-phosphate backbone can be done to facilitate the addition of additional moieties such as labels, or to increase the stability and half-life of such molecules in physiological environments, for example.

The term "specific hybridization" can refer to the binding, duplexing, or hybridizing of a nucleic acid molecule preferentially to a particular nucleotide sequence under stringent conditions, including conditions under which a probe can

hybridize preferentially to its target subsequence, and can hybridize to a lesser extent to other sequences.

The term "inhibitor of NELL peptides" refers to a chemical or biological compound capable of inhibiting the activity of NELL peptides. The term also includes a chemical or biological compound capable of suppressing the expression of NELL peptides. Inhibitors of NELL peptides can interact directly or indirectly with NELL peptide transcripts or translational products. As examples, methods of interactions can include but are not limited to decreased transcription or translation of NELL peptides, decreased stability of NELL peptide transcripts or protein products, decreased activity of NELL peptide transcripts or protein products, and increased degradation of NELL peptide transcript or protein products. The term "enhancer of NELL peptides" refers to a chemical or biological compound capable of enhancing the activity of NELL peptides. The term also includes a chemical or biological compound capable of enhancing the expression of NELL peptides. As examples, methods of interactions can include but are not limited to increased transcription or translation of NELL peptides, increased stability of NELL peptide transcripts or protein products, increased activity of NELL peptide transcripts or protein products, and decreased degradation of NELL peptide transcript or protein products.

The term "modulator of NELL peptide receptors" refers to a chemical or biological compound capable of facilitating or inhibiting the binding of NELL peptide receptors to or by NELL peptides or to a chemical or biological compound capable of modulating NELL peptide receptor activity irrespective of the presence or the absence of NELL peptide. The modulator that facilitates the binding and/or activation of NELL peptide receptors to or by NELL peptides is referred to as an "agonist" of the receptor, and the modulator that inhibits the binding and/or activation of NELL peptide receptors to or by NELL peptides is referred to as an "antagonist" of the receptor. The modulator that facilitates the activation of NELL peptide receptors irrespective of NELL peptides is referred to as an "activator" of the receptor, and the modulator that inhibits activation of NELL peptide receptors irrespective of NELL peptides is referred to as an "inhibitor" of the receptor.

The term "NELL peptide," "NELL related agent," "inhibitor of NELL peptide" or "modulator of NELL peptide receptor(s)" can also be referred to as an "agent" throughout the specification.

The term "delivery vehicle" refers to any delivery vehicle used in the art of biochemistry. Some examples of common delivery vehicle are a naked DNA type vehicle, an RNA type vehicle, a virus type vehicle. Some further examples are e.g., a polymer or a peptide, sustained release carriers, synthetic scaffolds, natural scaffolds, allograft or xenograft scaffolds.

The term "mammalian subject" or "mammal" refers to any mammals, examples of which include human beings and animals such as horse.

#### Cartilage Formation

Cartilage formation generally proceeds via chondrification process. Chondrification is the process in which cartilage is formed from condensed mesenchyme tissue, which differentiates into chondrocytes and begins secreting the materials that form the matrix. Cartilage can undergo mineralization. Adult hyaline articular cartilage, for example, is progressively mineralized at the junction between cartilage and bone. A mineralization front advances through the base of the hyaline articular cartilage at a rate dependent on cartilage load and shear stress. Intermittent variations in the rate of advance

and mineral deposition density of the mineralizing front lead to multiple tidemarks in the articular calcified cartilage.

Adult articular calcified cartilage is penetrated by vascular buds, and new bone produced in the vascular space in a process similar to endochondral ossification at the physis. A cement line demarcates articular calcified cartilage from subchondral bone. Two types of growth can occur in cartilage: appositional and interstitial. Appositional growth results in the increase of the diameter or thickness of the cartilage. The new cells derive from the perichondrium and occur on the surface of the cartilage model. Interstitial growth results in an increase of cartilage mass and occurs from within. Chondrocytes undergo mitosis within their lacuna but remain imprisoned in the matrix, which results in clusters of cells called isogenous groups.

Cartilage can also be formed via endochondral ossification. The mammalian skeleton develops through both endochondral and intramembranous bone formation processes. Embryologically, During skeletal development, the establishment of a layer of cartilage at the ends of certain bones is intimately linked to the process of endochondral ossification. The cartilaginous portion of endochondral bone formation involves chondroblast/chondrocyte differentiation, maturation, hypertrophy with or without mineralization depending on the location of the cartilage. Non-mineralizing cartilage formation includes but is not limited to formation of articular cartilage, temporomandibular joint, wrist, knee, and intervertebral disc fibrocartilages.

Endochondral ossification or long bone formation is related to bone formation, which permits functional stresses to be sustained during skeletal growth and is well demonstrated in the development of the long bones. In this process, a small model of the long bone is first formed in solid hyaline cartilage which undergoes mainly appositional growth to form an elongated, dumb-bell shaped mass of cartilage consisting of a shaft (diaphysis) and future articular portions (epiphysis) surrounded by perichondrium (see, e.g., Wheater, P. R. and H. G. Burkitt (1987). *Functional histology: a text and colour atlas*. Edinburgh; New York, Churchill Livingstone; Beaupre, G. S., S. S. Stevens, et al., *J Rehabil Res Dev* 37(2): 145-51) (2000)).

Within the shaft of the cartilage model then chondrocytes enlarge greatly, resorbing the surrounding cartilage so as to leave only slender perforated trabeculae of cartilage, matrix. This cartilage matrix then calcifies and the chondrocytes degenerate leaving large, interconnecting spaces. During this period the perichondrium of the shaft develops chondrogenic potential and assumes the role of periosteum. The periosteum then lays down a thin layer of bone around the surface of the shaft and primitive mesenchymal cells and blood vessels invade the spaces left within the shaft after degeneration of the chondrocytes. The primitive mesenchymal cells differentiate into osteoblasts and blood-forming cells on the surface of the calcified remnants of the cartilage matrix and commence the formation of irregular, woven bone (Wheater and Burkitt, 1987, supra). In the cartilage model described in Wheater and Burkitt, 1987, supra, the ends of the original cartilage model have then become separated by a large site of primary ossification in the shaft. The cartilaginous ends of the model, however, continue to grow in diameter. Meanwhile, the cartilage at the ends of the shaft continues to undergo regressive changes followed by ossification so that the developing bone now consists of an elongated, bony diaphyseal shaft with a semilunar cartilage epiphysis at each end. The interface between the shaft and each epiphysis constitutes a growth or epiphyseal plate. Within the growth plate, the cartilage proliferates continuously, resulting in progressive elon-

gation of the bone. At the diaphyseal aspect of each growth plate, the chondrocytes mature and then die, the degenerating zone of cartilage being replaced by bone. Thus the bony diaphysis lengthens and the growth plates are pushed further and further apart. On reaching maturity, hormonal changes inhibit further cartilage proliferation and the growth plates are replaced by bone causing fusion of the diaphysis and epiphysis (Wheater and Burkitt, 1987, supra). In the meantime, in the center of the mass of cartilage of each developing epiphysis, regressive changes and bone formation similar to that in the diaphyseal cartilage occur along with appositional growth of cartilage over the whole external surface of the epiphysis. This conversion of central epiphyseal cartilage to bone is known as secondary ossification. A thin zone of hyaline cartilage always remains at the surface as the articular cartilage (Wheater and Burkitt, 1987, supra).

Thus, endochondral bone formation and growth is achieved in part by the proliferation and maturation of cartilage cells (chondroblasts, chondrocytes) with or without cartilage cell mineralization. Cartilage formation or regeneration can be achieved by controlling cartilage cell mineralization. Without being bound by a particular theory, cartilage cell mineralization can be controlled by controlling factors such as: a) location, b) cell type, c) cell differentiation state, d) microenvironment, and e) biomechanical forces. For example, the mineralization of a cartilage cell can be controlled by placing the cartilage cell near an epiphyseal growth plate in which mineralization generally occurs or near an articular surface in which mineralization generally does not occur. It is known in the art that chondrocyte hypertrophy and up-regulated matrix calcification are dissociable states (see, e.g., Johnson, van Etten et al. 2003) (see, e.g., Johnson, K. A., D., et al., *J Biol Chem* 278(21):18824-32 (2003)). For example, the formation of endochondral bone can be evaluated by chondroblast hypertrophy as viewed by an increase in hypertrophic and apoptotic chondroblasts, elucidated by TUNEL staining. In another example, the formation of cartilage can be evaluated also by chondroblast hypertrophy without necessarily apoptosis or mineralization.

#### Cartilage Regeneration

Cartilage contains a significant amount of water. For instance, articular cartilage is comprised of mostly water (60-80 wt %) and the remaining ECM comprises mostly type II collagen (50-90% dry mass) and proteoglycans (5-10%). Other collagens and minor ECM molecules have been identified in small quantities. It is organization of the ECM into distinct zones, and the interaction between water and the ECM in the various zones that provide the toughness that is required for the absorption and transmission of biomechanical forces across joints, and simultaneously the frictionless articulating surfaces that are needed for joint motion. Stresses as high as 4 and 20 MPa have been reported in human hip joints during routine walking and jumping, respectively! As amazing as the articular cartilage is, it exhibits unfortunately minimal capacity for repair. Over 20 million Americans suffer from osteoarthritis and degenerative joint diseases with an associated annual healthcare burden of over \$60 billion. A wide array of scaffolds, cytokines, and growth factors have been investigated for cartilage tissue engineering (see, e.g., Frenkel, S. R., et al., *Ann. Biomed. Eng.* 32:26-34 (2004); Tuli, R., et al., *Arthritis Res. Ther.* 5:235-238 (2003); and Ashammakhi, N. and Reis, R.L. *Topics in Tissue Engineering*, Vol. 2, 2005). The role of static vs. dynamic compression, shear stress, hydrostatic pressure, fluid flow, electrical streaming potentials, bioreactors, and complex loading on

chondrocyte biological response and tissue remodeling have been investigated extensively and the mechanotransduction pathways reviewed Ashammakhi, N. and Reis, R L. Topics in Tissue Engineering, Vol. 2, 2005) (see FIGS. 7A-D therein)

Accordingly, in a further aspect of the present invention, the composition provided herein includes at least a NELL peptide or an agonist of the receptor of NELL peptides in an amount effective for inducing chondroblast and chondrocyte to form cartilage. NELL proteins, peptides, DNA, RNA, and NELL agonists, and antagonist inhibitors can be used alone or in conjunction with scaffolds with and without cells, with or without mechanical stimulation, in the presence or absence of additional growth factors. For example, in one embodiment, the composition can be effective in regenerating or repairing or augmenting cartilage in intervertebral disc, temporomandibular disc, knee and wrist fibrocartilage, and articular surfaces. In another embodiment, the composition can be effective in forming cartilage via ex vivo gene therapy and protein application to cells with or without scaffold in tissue engineering.

Depending on the delivery method and the local environment, a composition including a NELL peptide (e.g., a NELL1 peptide) can be used to induce an chondrogenic cell, as such as a chondrocyte or chondroblast, to differentiate and form cartilage only. For example, in an articular cartilage defect, the composition described herein can induce an chondrogenic cell such as chondrocyte/blast to form cartilage only. The composition can be applied to the defected cartilage area as a scaffold/carrier. In some embodiments, the composition can optionally include cells (stem cells, chondroblast etc). In some embodiments, the composition can be applied as gene therapy.

In some embodiments, as used herein, the cells can be, e.g., differentiated chondrocytes; differentiated cells (e.g. skeletal muscle cells, fibroblasts) that are de-differentiated after implantation, or prior to implantation; adult stem cells that are differentiated after implantation, or prior to implantation; embryonic stem cells that are differentiated after implantation, or prior to implantation; human; modified by nucleic acid, protein, small molecules, siRNA, antibodies.

In some yet embodiments, the composition can be used in cartilage tissue engineering. For example, when chondroblasts are cultured on an "oscillating", intermittent stress tension environment, NELL1 peptide can include the chondroblast cells to differentiate and form cartilage. In these embodiments, the duration of application of the oscillating stress also plays an important role. For example, if the oscillating force is applied continuously, the composition having a NELL1 peptide can induce endochondral bone formation. Therefore, in the application of the oscillating stress shall be intermittently such that the differentiation of an chondrogenic cell (e.g., chondrocyte/blast) can stop at the cartilage stage and thus prevent the cell from differentiating into endochondral bone formation.

Therefore, in some embodiments, the composition described herein can be used to regenerate/repair cartilage, e.g., for disc repair in articular cartilage and intervertebral disc.

Other exemplary cartilage conditions that can be treated, prevented, or ameliorated by a composition disclosed herein include, but are not limited to, chondrocalcinosis, osteoarthritis, and/or other diseases characterized by pathological cartilage degeneration.

In one embodiment, a method of increasing endochondral bone formation can include increasing the concentration of a NELL1 gene product in a region where bone formation is desired; optionally applying a second agent to the region

where bone formation is desired and at least inducing hypertrophy of chondroblast in the region where bone formation is desired.

The method can include increasing the concentration of a NELL1 gene product by applying a NELL1 peptide to the location where bone formation is desired, and the NELL1 peptide can be selected from the group comprising: SEQ ID NO:2, SEQ ID NO: 4, or SEQ ID NO:6, or any portion of the NELL peptide which is effective in increasing endochondral bone formation, which involves both cartilage and bone.

The second agent can include, but is not limited to TGF-beta, BMP2, BMP4, BMP7, bFGF, insulin like growth factor (IGF), Sox9, collagen, chondrogenic cells, bone, bone matrix, tendon matrix, ligament matrix. The second agent can be selected to have a complimentary or synergistic effect with NELL1 in inducing endochondral bone formation. Other agents are described below.

#### Inhibition of Angiogenesis and Cartilage Formation/Regeneration

As specified in Shukunami et al., cartilage forms a template for most of the bony skeleton in embryonic development (Shukunami, C., Y. Oshima, et al., Biochem Biophys Res Commun 333(2): 299-307) (2005)). Cartilage is not directly converted to bone but is gradually replaced through the actions of osteoclasts and osteoblasts, which are brought to the ossification center of cartilage with vascular invasion (endochondral bone formation). Thus, the vascular invasion of cartilage can be crucial for bone formation at an appropriate stage of development. Cartilage acquires an anti-angiogenic nature upon chondrogenesis and quickly loses it, as chondrocytes mature to become hypertrophic and calcified prior to vascular invasion, suggesting that cartilage undergoes a dynamic switching of the anti-angiogenic phenotype. Undoubtedly pro-angiogenic factors act as a driving force for vascular invasion into tissues. VEGF-A is a key regulator of angiogenesis during endochondral bone formation: VEGF-A is expressed in hypertrophic cartilage, but not in resting or proliferating cartilage.

Matrix metalloproteinases (MMPs) can influence bone development, which involves matrix-remodeling during vascular invasion (e.g., MMP-9, MMP-13, MMP-14). In mice lacking MMP-9, vascular invasion and subsequent ossification were delayed, causing progressive lengthening of the growth plate. The delay in ossification appeared to be secondary to a diminished vascular invasion of cartilage probably because MMP-9-deficient hypertrophic cartilage fails to release normal levels of pro-angiogenic activity to stimulate vessel formation and to recruit osteo/chondroclasts. Targeted inactivation of MMP-14 (membrane type 1 MMP: MT1-MMP) causes severe defects in both endochondral and intramembranous bone formation in mice. These results indicate that MMPs play a regulatory role in angiogenic switching of the cartilage phenotype. Thus, an important part of cartilage formation and regeneration can involve differential regulation of pro-angiogenic factors such as MMP-9, MMP-13, MMP-14, and VEGF and anti-angiogenic factors such as chondromodulin-I (ChM-I), thrombospondin (TSP)-1, TSP-2, tissue inhibitor of metalloproteinase (TIMP)-2, TIMP-3. Specifically, pro-angiogenic factors can be relatively more prominent in areas of cartilage undergoing ossification, and anti-angiogenic factors may be relatively more prominent in areas of cartilage not undergoing ossification. These results also indicate that the transcription factor Cbfa1/Runx2 can be involved in the control of angiogenic switching in cartilage: Cbfa1/Runx2 null mice are defective in hypertrophic carti-

lage differentiation, vascular invasion of cartilage rudiments, and VEGF expression, and exhibit a sustained expression of the ChM-I gene. In Cbfa1/Runx2 null mice expressing the Cbfa1/Runx2 transgene in non hypertrophic chondrocytes, vascular invasion, and cartilage remodeling was restored with the upregulation of VEGF and concomitant downregulation of ChM-I gene expression.

Without being bound by a particular theory, NELL1 can have a role in the angiogenic switching in cartilage, since NELL1 is a direct downstream effector of Cbfa1/Runx2 effects. In addition without being bound by a particular theory, NELL1's role in cartilage formation can also relate to potential anti-angiogenic effects of NELL1—as NELL1 also contains a NH<sub>2</sub>-terminal thrombospondin-like module.

#### Other Agents

In one embodiment, the composition for cartilage formation and regeneration described herein can include one or more other agents. Such agents can be chondroprotective agents, anti-pain and/or anti-inflammatory agents, growth factors, anti-angiogenic agents, or combinations thereof.

The chondroprotective agents can be, for example, (1) antagonists of receptors for the interleukin-1 family of proteins, including, for example, IL-1.beta., IL-17 and IL-18; (2) antagonists of the tumor necrosis factor (TNF) receptor family, including, for example, TNF-R1; (3) agonists for interleukin 4, 10 and 13 receptors; (4) agonists for the TGF-.beta. receptor superfamily, including, for example, BMP-2, BMP-4 and BMP-7; (5) inhibitors of COX-2; (6) inhibitors of the MAP kinase family, including, for example, p38 MAP kinase; (7) inhibitors of the matrix metalloproteinases (MMP) family of proteins, including, for example, MMP-3 and MMP-9; (8) inhibitors of the NF-.kappa.B family of proteins, including, for example, the p50/p65 dimer complex with I.kappa.B; (9) inhibitors of the nitric oxide synthase (NOS) family, including, for example, iNOS; (10) agonists and antagonists of integrin receptors, including, for example, agonists of  $\alpha_v\beta_3$  integrin; (11) inhibitors of the protein kinase C (PKC) family; (12) inhibitors of the protein tyrosine kinase family, including, for example, the src subfamily; (13) modulators of protein tyrosine phosphatases; and (14) inhibitors of protein src homology 2 (SH2) domains. Additional chondroprotective agents include other growth factors, such as by way of example insulin-like growth factors (e.g., IGF-1) and fibroblast growth factors (e.g., bFGF). Other chondroprotective agents are described in U.S. Pat. No. 7,067,144, the teachings of which are incorporated herein by reference. These chondroprotective agents can be used alone or in combination along with a NELL peptide or related agent. In some embodiments, the composition described herein can specifically exclude any of the above described chondroprotective agents.

The anti-pain and/or anti-inflammatory agents can be, e.g., (1) serotonin receptor antagonists; (2) serotonin receptor agonists; (3) histamine receptor antagonists; (4) bradykinin receptor antagonists; (5) kallikrein inhibitors; (6) tachykinin receptor antagonists, including neurokinin.sub.1 and neurokinin.sub.2 receptor subtype antagonists; (7) calcitonin gene-related peptide (CGRP) receptor antagonists; (8) interleukin receptor antagonists; (9) inhibitors of enzymes active in the synthetic pathway for arachidonic acid metabolites, including (a) phospholipase inhibitors, including PLA.sub.2 isoform inhibitors and PLC isoform inhibitors, (b) cyclooxygenase inhibitors, and (c) lipoxygenase inhibitors; (10) prostanoid receptor antagonists including eicosanoid EP-1 and EP-4 receptor subtype antagonists and thromboxane receptor subtype antagonists; (11) leukotriene receptor

antagonists including leukotriene B.sub.4 receptor subtype antagonists and leukotriene D.sub.4 receptor subtype antagonists; (12) opioid receptor agonists, including  $\mu$ -opioid,  $\delta$ -opioid, and  $\kappa$ -opioid receptor subtype agonists; (13) purinoceptor antagonists including P<sub>2</sub>X receptor antagonists and P<sub>2</sub>Y receptor antagonists; and (14) calcium channel antagonists. Each of the above agents functions either as an anti-inflammatory agent and/or as an anti-nociceptive (i.e., anti-pain or analgesic) agent. The selection of agents from these classes of compounds is tailored for the particular application. These anti-pain and/or anti-inflammatory agents can be used alone or in combination along with a NELL peptide or related agent. In some embodiments, the composition described herein can specifically exclude any of the above described anti-pain and/or anti-inflammatory agents.

The growth factors can be, e.g., FGF-2, FGF-5, IGF-1, TGF-.beta., BMP-2, BMP-7, PDGF, VEGF, OP1, OP2, OP3, BMP2, BMP3, BMP4, BMP5, BMP6, BMP9, BMP10, BMP11, BMP12, BNP15, BMP16, DPP, Vgl, 60A protein, GDF-1, GDF3, GDF5, GDF6, GDF7, GDF8, GDF9, GDF10 and GDF11. Some other growth factors are described in U.S. Pat. Nos. 7,067,123, and 7,041,641, the teachings of which are incorporated herein by reference. These growth factors can be used alone or in combination along with a NELL peptide or related agent. In some embodiments, the composition described herein can specifically exclude any of the above described growth factors.

The anti-angiogenic agents can be, e.g., anti-angiogenic factors, including for example Anti-Invasive Factor, retinoic acids and their derivatives, paclitaxel including analogues and derivatives thereof, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator Inhibitor-1 and Plasminogen Activator Inhibitor-2, and lighter "d group" transition metals. Similarly, a wide variety of polymeric carriers may be utilized, representative examples of which include poly(ethylene-vinyl acetate) (40% cross-linked), poly(D,L-lactic acid) oligomers and polymers, poly(L-lactic acid) oligomers and polymers, poly(glycolic acid), copolymers of lactic acid and glycolic acid, poly(caprolactone), poly(valerolactone), poly(anhydrides), copolymers of poly(caprolactone) or poly(lactic acid) with polyethylene glycol, and blends thereof. Within certain preferred embodiments, the compositions comprise a compound which disrupts microtubule function, such as, for example, paclitaxel, estramustine, colchicine, methotrexate, curacin-A, epothilone, vinblastine or tBCEV. Within other preferred embodiments, the compositions comprise a polymeric carrier and a lighter d group transition metal (e.g., a vanadium species, molybdenum species, tungsten species, titanium species, niobium species or tantalum species) which inhibits the formation of new blood vessels (as specified in USP 20060240113), inhibitors of VEGF (as specified in USP 20060241084), other inhibitors of angiogenesis (as specified in USP 20060235034, U.S. Pat. No. 7,122,635), chondromodulin-I or tenomodulin (Shukunami, et al., 2005, supra), or other endogenous or exogenous anti-angiogenic factors well known to those in the art.

#### Formulations

The composition described herein can be formulated into any desired formulation. The composition can include materials and carriers to effect a desired formulation. For example, the composition can include an injectable or moldable material that can set within a pre-defined period of placement. Such a pre-defined period can be, e.g., 10 minutes, 30 minutes, one hour, two hours, etc.

In some embodiments, the composition can include a chemical gel that includes primary bonds formed due to changes in pH, ionic environment, and solvent concentration. Examples of such chemical gels can be, but are not limited to, polysaccharides such as chitosan, chitosan plus ionic salts such as beta-glycerophosphates, aginates plus Ba<sup>2+</sup>, Sr<sup>2+</sup>, Ca<sup>2+</sup>, Mg<sup>2+</sup>, collagen, fibrin, plasma or combinations thereof.

In some embodiments, the composition can include a physical gel that include secondary bonds formed due to temperature changes. Examples of such physical gels can be, but are not limited to, alginate, poly(ethylene glycol)-poly(lactic acid-co-glycolic acid)-poly(ethylene glycol) (PEG-PLGA-PEG) tri-block copolymers, agarose, and celluloses. In some embodiments, physical gels that can be used in the composition described herein can include physical gels that are liquid under high shear but gels to solid at low shear. Examples of such physical gels include, but are not limited to, hyaluronic acid, or polyethylene oxides. The physical gels can have pre-formed materials with pre-defined dimensions and shape.

In some embodiments, the composition described herein can include a material that degrade or release active agents in response to a stimulus. Some examples of such stimuli are mechanical stimuli, light, temperature changes, pH changes, change of ionic strength, or electromagnetic field. Such materials are know in the art. some examples of such materials are chitosan, alginates, pluronics, methyl cellulose, hyaluronic acids, and polyethylene oxides. Other examples are described by Brandi F, Sommer F, Goepferich A. "Rational design of hydrogels for tissue engineering: Impact of physical factors on cell behavior" in *Biomaterials*. Epub 2006 Sep. 29.

In some embodiments, the composition described herein can include a gel containing any of hydroxyapatites, apatites, tricalcium phosphates, calcium phosphates, bioactive glass, human allograft bone and cartilage, bovine bone and cartilage, or their mixtures thereof.

In some embodiments, the composition described herein including any of the gels described above can further include a crosslinker to further tailor degradation kinetics and controlled release. Alternatively, in some embodiments, the composition described herein can include an interpenetrating phase composite or interpenetrating network (IPN) that includes any of the above described gels. Some examples of the crosslinker includes, but are not limited to, common crosslinking agents (polyalkylene oxide, ethylene dimethacrylate, N,N'-methylenebisacrylamide, methylenebis(4-phenyl isocyanate), ethylene dimethacrylate, divinylbenzene, allyl methacrylate, carbodiimidazole, sulfonyl chloride, chlorocarbonates, n-hydroxysuccinimide ester, succinimidyl ester, epoxides, aryl halides, sulfasuccinimidyl esters, and maleimides); PEG based crosslinkers (e.g. MAL-dPEGx-NHS-esters, MAL-dPEGx acid, Bis-MAL-dPEGx, etc.) and photo/light activated crosslinkers, N-hydroxysuccinimide-based crosslinkers, dilysine, trilysine, and tetralysine.

The composition described herein can include a carrier. The carrier can be a polymeric carrier or non-polymeric carrier. In some embodiments, the carrier can be biodegradable, such as degradable by enzymatic or hydrolytic mechanisms. Examples of carriers include, but are not limited to synthetic absorbable polymers such as but not limited to poly( $\alpha$ -hydroxy acids) such as poly(L-lactide) (PLLA), poly(D, L-lactide) (PDLLA), polyglycolide (PGA), poly(lactide-co-glycolide) (PLGA), poly(-caprolactone), poly(trimethylene carbonate), poly(p-dioxanone), poly(-caprolactone-co-glycolide), poly(glycolide-co-trimethylene carbonate) poly(D,

L-lactide-co-trimethylene carbonate), polyarylates, polyhydroxybutyrate (PHB), polyanhydrides, poly(anhydride-co-imide), propylene-co-fumarates, polylactones, polyesters, polycarbonates, polyanionic polymers, polyanhydrides, polyester-amides, poly(amino-acids), homopolypeptides, poly(phosphazenes), poly(glaxanone), polysaccharides, and poly(orthoesters), polyglactin, polyglactic acid, polyaldonic acid, polyacrylic acids, polyalkanoates; copolymers and admixtures thereof, and any derivatives and modifications. See for example, U.S. Pat. No. 4,563,489, and PCT Int. Appl. No. WO/03024316, herein incorporated by reference. Other examples of carriers include cellulosic polymers such as, but not limited to alkylcellulose, hydroxyalkylcellulose, methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, carboxymethylcellulose, and their cationic salts. Other examples of carriers include synthetic and natural bioceramics such as, but not limited to calcium carbonates, calcium phosphates, apatites, bioactive glass materials, and coral-derived apatites. See for example U.S. Patent Application 2002187104; PCT Int. Appl. WO/9731661; and PCT Int. Appl. WO/0071083, herein incorporated by reference.

In one embodiment, the carrier can further be coated by compositions, including bioglass and or apatites derived from sol-gel techniques, or from immersion techniques such as, but not limited to simulated body fluids with calcium and phosphate concentrations ranging from about 1.5 to 7-fold the natural serum concentration and adjusted by various means to solutions with pH range of about 2.8-7.8 at temperature from about 15-65 degrees C. See, for example, U.S. Pat. Nos. 6,426,114 and 6,013,591; and PCT Int. Appl. WO/9117965 herein incorporated by reference.

Other examples of carriers include, collagen (e.g. Collastat, Helistat collagen sponges), hyaluronan, fibrin, chitosan, alginate, and gelatin. See for example, PCT Int. Appls. WO/9505846; WO/02085422, herein incorporated by reference.

In one embodiment, the carrier can include heparin-binding agents; including but not limited to heparin-like polymers e.g. dextran sulfate, chondroitin sulfate, heparin sulfate, fucan, alginate, or their derivatives; and peptide fragments with amino acid modifications to increase heparin affinity. See for example, *Journal of Biological Chemistry* (2003), 278(44), p. 43229-43235, herein incorporated by reference.

In one embodiment, the composition can be in the form of a liquid, solid or gel. In one embodiment, the substrate can include a carrier that is in the form of a flowable gel. The gel can be selected so as to be injectable, such as via a syringe at the site where cartilage formation is desired. The gel can be a chemical gel which can be a chemical gel formed by primary bonds, and controlled by pH, ionic groups, and/or solvent concentration. The gel can also be a physical gel which can be formed by secondary bonds and controlled by temperature and viscosity. Examples of gels include, but are not limited to, pluronics, gelatin, hyaluronan, collagen, polylactide-polyethylene glycol solutions and conjugates, chitosan, chitosan & b-glycerophosphate (BST-gel), alginates, agarose, hydroxypropyl cellulose, methyl cellulose, polyethylene oxide, polylactides/glycolides in N-methyl-2-pyrrolidone. See for example, *Anatomical Record* (2001), 263(4), 342-349, herein incorporated by reference.

In one embodiment, the carrier can be photopolymerizable, such as by electromagnetic radiation with wavelength of at least about 250 nm. Example of photopolymerizable polymers include polyethylene (PEG) acrylate derivatives, PEG methacrylate derivatives, propylene fumarate-co-ethylene glycol, polyvinyl alcohol derivatives, PEG-co-poly(-hydroxy

acid) diacrylate macromers, and modified polysaccharides such as hyaluronic acid derivatives and dextran methacrylate. See for example, U.S. Pat. No. 5,410,016, herein incorporated by reference.

In one embodiment, the substrate can include a carrier that is temperature sensitive. Examples include carriers made from N-isopropylacrylamide (NiPAM), or modified NiPAM with lowered lower critical solution temperature (LCST) and enhanced peptide (e.g. NELL1) binding by incorporation of ethyl methacrylate and N-acryloxysuccinimide; or alkyl methacrylates such as butylmethacrylate, hexylmethacrylate and dodecylmethacrylate. PCT Int. Appl. WO/2001070288; U.S. Pat. No. 5,124,151 herein incorporated by reference. In one embodiment, where the carrier can have a surface that is decorated and/or immobilized with cell adhesion molecules, adhesion peptides, and adhesion peptide analogs which can promote cell-matrix attachment via receptor mediated mechanisms, and/or molecular moieties which can promote adhesion via non-receptor mediated mechanisms binding such as, but not limited to polycationic polyamino-acid-peptides (e.g. poly-lysine), polyanionic polyamino-acid-peptides, Mefp-class adhesive molecules and other DOPA-rich peptides (e.g. poly-lysine-DOPA), polysaccharides, and proteoglycans. See for example, PCT Int. Appl. WO/2004005421; WO/2003008376; WO/9734016, herein incorporated by reference.

In one embodiment, the carrier can include various naturally occurring matrices or their components such as devitalized cartilage matrix, demineralized bone matrix, or other components derived from allograft, xenograft, or any other naturally occurring material derived from Monera, Protista, Fungi, Plantae, or Animalia kingdoms.

In one embodiment, the carrier can include comprised of sequestering agents such as, but not limited to, collagen, gelatin, hyaluronic acid, alginate, poly(ethylene glycol), alkylcellulose (including hydroxyalkylcellulose), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, blood, fibrin, polyoxyethylene oxide, calcium sulfate hemihydrate, apatites, carboxyvinyl polymer, and poly(vinyl alcohol). See for example, U.S. Pat. No. 6,620,406, herein incorporated by reference.

In one embodiment, the carrier can include surfactants to promote NELL1 stability and/or distribution within the carrier materials such as, but not limited to polyoxyester (e.g. polysorbate 80, polysorbate 20 or Pluronic F-68).

In one embodiment, the carrier can include buffering agents such as, but not limited to glycine, glutamic acid hydrochloride, sodium chloride, guanidine, heparin, glutamic acid hydrochloride, acetic acid, succinic acid, polysorbate, dextran sulfate, sucrose, and amino acids. See for example, U.S. Pat. No. 5,385,887, herein incorporated by reference. In one embodiment, the carrier can include a combination of materials such as those listed above. By way of example, the carrier can be a PLGA/collagen carrier membrane. The membrane can be soaked in a solution including NELL1 peptide.

In one embodiment, an implant for use in the human body can include a substrate including NELL1 in an amount sufficient to induce cartilage formation or repair proximate to the implant.

In one embodiment, an implant for use in the human body can include a substrate having a surface including NELL1 in an amount sufficient to induce cartilage formation or repair proximate to the implant.

In one embodiment, an implant for use in the human body can include a substrate having a surface including chondro-

genic cells, and NELL1 in an amount sufficient to induce cartilage formation or repair. In one embodiment, the implant can be seeded with cells, including but not limited to autologous cells, chondrogenic or osteoblastic cells, cells expressing NELL1 or another chondrogenic molecule.

An implant can include a substrate formed into the shape of a mesh, pin, screw, plate, or prosthetic joint. By way of example, a substrate can be in a form of a dental or orthopedic implant, and NELL1 can be used to enhance integration in bone in proximity to the implant. An implant can include a substrate that is resorbable, such as a substrate including collagen.

The NELL1 peptide can be combined with a acceptable carrier to form a pharmacological composition. Acceptable carriers can contain a physiologically acceptable compound that acts, for example, to stabilize the composition or to increase or decrease the absorption of the agent. Physiologically acceptable compounds can include, for example, carbohydrates, such as glucose, sucrose, or dextrans, antioxidants, such as ascorbic acid or glutathione, chelating agents, low molecular weight proteins, compositions that reduce the clearance or hydrolysis of the anti-mitotic agents, or excipients or other stabilizers and/or buffers.

Other physiologically acceptable compounds include wetting agents, emulsifying agents, dispersing agents or preservatives which are particularly useful for preventing the growth or action of microorganisms. Various preservatives are well known and include, for example, phenol and ascorbic acid. One skilled in the art would appreciate that the choice of a carrier, including a physiologically acceptable compound depends, for example, on the route of administration.

The compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable can include powder, or injectable or moldable pastes or suspension.

The compositions of this invention can comprise a solution of the NELL1 peptide dissolved in a pharmaceutically acceptable carrier, such as an aqueous carrier for water-soluble peptides. A variety of carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions can be sterilized by conventional, well known sterilization techniques. The compositions can contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, for example, sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like.

The concentration of NELL1 peptide in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs.

The dosage regimen will be determined by the clinical indication being addressed, as well as by various patient variables (e.g. weight, age, sex) and clinical presentation (e.g. extent of injury, site of injury, etc.).

However, a therapeutically effective dose of a NELL1 peptide or agent useful in this invention is one which has a positive clinical effect on a patient or desired effect in cells as measured by the ability of the agent to enhance chondrogenic differentiation for cartilage formation or repair, as described above. The therapeutically effective dose of each peptide or agent can be modulated to achieve the desired clinical effect, while minimizing negative side effects. The dosage of the peptide or agent can be selected for an individual patient depending upon the route of administration, severity of the



disease, age and weight of the patient, other medications the patient is taking and other factors normally considered by an attending physician, when determining an individual regimen and dose level appropriate for a particular patient.

#### Device

The composition can be formulated into an injectable or implantable device in any desired form. Some exemplary devices can be for intervertebral disc nucleus replacement, knee meniscus replacement, wrist triangular fibrocartilage replacement, temporomandibular joint replacement, articular cartilage replacement and can consist of, porous scaffold with preformed shape and attachment features to anchor to underlying bone; viscous gel with preformed shape that can be re-shaped by manual manipulation and the cured to new shape by the application of light; or low viscosity liquid that can polymerize in situ. For example, the composition can be formulated into a single mixture (or a simple mixture) for cartilage formation.

In some embodiments, the composition can be formulated into a single device containing specifically designed layers that are tissue-specific, e.g. it may be desirable to have a bone layer to anchor to the hard tissues, and then a cartilage layer immediately adjacent to the bone layer.

In some embodiments, the composition can be formulated into a single mixture allowing multiple tissues formation and self-assembly, such as. polymers or monomers with amphiphilic functional groups can self-assemble into macroscopic structures.

In some embodiments, where a device including a composition described herein having a cell(s), the device can be subjected to pre-implantation stimulation. For example, the device can be placed in a mechanical bioreactor with controlled mechanical stimulation (frequency, duty cycle, amplitude, etc.); Frequency in the range of 0.01 Hz to 10,000 Hz, duty cycle above 10%; and amplitude in the range of 0.1-100% strain have reported enhanced cellular function. In some embodiments, the device described herein can be placed in a mechanical bioreactor with controlled microfluidic flow and shear stresses, which arise when at least one flow path or channel has one dimension less than 1 mm. In some embodiments, a device described herein can be implanted in a human being via direct implantation immediately following cell harvesting.

In some embodiments, the composition provided herein can form any of the following examples of devices, which illustrate, but shall not be construed to limit the claimed invention:

An injectable/implantable device containing NELL protein (with or without cells) that can be directly injected/implanted into spinal discs to promote cartilage formation;

A disc nucleus replacement device impregnated with NELL that is designed to replace the inner portion of the vertebral disc (the nucleus) or both the inner and outer portion of the disc;

An injectable/implantable device containing NELL (with or without cells) that can be directly injected into the various joint spaces (e.g., knee, temporomandibular joint, wrist) or implanted arthroscopically or openly into various joint spaces;

An injectable/implantable device containing NELL nucleic acids (with or without delivery vehicle such as a virus) (with or without cells) that can be directly injected/implanted into spinal discs to promote cartilage formation;

A disc nucleus replacement device impregnated with NELL nucleic acids (with or without delivery vehicle such as

a virus) that is designed to replace the inner portion of the vertebral disc (the nucleus) or both the inner and outer portion of the disc;

5 An injectable/implantable device containing NELL nucleic acids (with or without delivery vehicle such as a virus) (with or without cells) that can be directly injected into the various joint spaces (e.g., knee, temporomandibular joint, wrist) or implanted arthroscopically or openly into various joint spaces;

10 An injectable/implantable device containing NELL protein (with or without cells) and other factors that can be directly injected/implanted into spinal discs to promote cartilage formation;

15 A disc nucleus replacement device impregnated with NELL and other factors that is designed to replace the inner portion of the vertebral disc (the nucleus) or both the inner and outer portion of the disc;

20 An injectable/implantable device containing NELL and other factors (with or without cells) that can be directly injected into the various joint spaces (e.g., knee, temporomandibular joint, wrist) or implanted arthroscopically or openly into various joint spaces;

25 An injectable/implantable device containing NELL nucleic acids and other factors (with or without delivery vehicle such as a virus) (with or without cells) that can be directly injected/implanted into spinal discs to promote cartilage formation;

30 A disc nucleus replacement device impregnated with NELL nucleic acids (with or without delivery vehicle such as a virus) that is designed to replace the inner portion of the vertebral disc (the nucleus) or both the inner and outer portion of the disc;

35 An injectable/implantable device containing NELL nucleic acids (with or without delivery vehicle such as a virus) (with or without cells) that can be directly injected into the various joint spaces (e.g., knee, temporomandibular joint, wrist) or implanted arthroscopically or openly into various joint spaces.

#### Dosages

Dosages of NELL peptides and other agents can be determined according to methods known in the art based on type of agent, the disease, and other factors such as age and gender.

45 In one embodiment, the dosage of NELL peptide for cartilage formation or repair generally ranges from 0.001  $\text{pg/mm}^2$  to 1  $\text{pg/mm}^2$ , or more preferably from 0.001  $\text{ng/mm}^2$  to 1  $\text{ng/mm}^2$ , or more preferably from 0.001  $\mu\text{g/mm}^2$  to 1  $\mu\text{g/mm}^2$ , or more preferably from 0.001  $\text{mg/mm}^2$  to 1  $\text{mg/mm}^2$ , or more preferably from 0.001  $\text{g/mm}^2$  to 1  $\text{g/mm}^2$ , with or without a particular carrier or scaffold. In another embodiment, the dosage of NELL peptide for cartilage formation or repair generally ranges from 0.001  $\text{pg/ml}$  to 1  $\text{pg/ml}$ , or more preferably from 0.001  $\text{ng/ml}$  to 1  $\text{ng/ml}$ , or more preferably from 0.001  $\mu\text{g/ml}$  to 1  $\mu\text{g/ml}$ , or more preferably from 0.001  $\text{mg/ml}$  to 1  $\text{mg/ml}$ , or more preferably from 0.001  $\text{g/ml}$  to 100  $\text{g/ml}$ , with or without a particular carrier or scaffold. In yet another embodiment, the dosage of NELL peptide for cartilage formation or repair generally ranges from 0.001  $\text{pg/kg}$  to 1  $\text{pg/kg}$ , or more preferably from 0.001  $\text{ng/kg}$  to 1  $\text{ng/kg}$ , or more preferably from 0.001  $\mu\text{g/kg}$  to 1  $\mu\text{g/kg}$ , or more preferably from 0.001  $\text{mg/kg}$  to 1  $\text{mg/kg}$ , or more preferably from 0.001  $\text{gm/kg}$  to 1  $\text{gm/kg}$ , more preferably from 0.001  $\text{kg/kg}$  to 1  $\text{kg/kg}$  with or without a particular carrier or scaffold. Furthermore, it is understood that all dosages can be continuously given or divided into dosages given per a given timeframe. Examples of timeframes include but

are not limited to every 1 hour, 2 hour, 4 hour, 6 hour, 8 hour, 12 hour, 24 hour, 48 hour, or 72 hour, or every week, 2 weeks, 4 weeks, or every month, 2 months, 4 months, and so forth.

However, because NELL peptides can have effects on in vitro osteoblast apoptosis (Zhang, X., et al., *J Bone Miner Res*, 2003. 18(12): p. 2126-34), NELL dosages (e.g., NELL1 dosages) that are significantly above an optimal range can not increase cartilage formation or repair. Accordingly, even more preferable dosages of NELL peptide shall not be significantly above the optimal dosage range. The even more preferable optimal dosage ranges of NELL peptides can vary according to factors such as the type, the age, the location, and the gender of a mammalian subject; the carrier or scaffold material employed; and the purity and potency of different NELL peptides. In one embodiment, the even more preferable optimal dosage ranges of NELL peptides includes but are not limited to 1 ng/mm<sup>2</sup> to 100 ng/mm<sup>2</sup>, or even more preferably from 100 ng/mm<sup>2</sup> to 1000 ng/mm<sup>2</sup>, or even more preferably from 1 μg/mm<sup>2</sup> to 100 μg/mm<sup>2</sup>, or even more preferably from 100 μg/mm<sup>2</sup> to 1000 μg/mm<sup>2</sup>. In another embodiment, the even more preferable optimal dosage ranges of NELL peptides includes but are not limited to 1 ng/ml to 100 ng/ml, or even more preferably from 100 ng/ml to 1000 ng/ml, or even more preferably from 1 μg/ml to 100 μg/ml, or even more preferably from 100 μg/ml to 1000 μg/ml. In yet another embodiment, even more preferable optimal dosage ranges of NELL peptide for cartilage formation or repair generally ranges from 1 μg/kg to 100 μg/kg, or even more preferably from 100 μg/kg to 1000 μg/kg, or even more preferably from 1 mg/kg to 100 mg/kg with or without a particular carrier or scaffold. Furthermore, it is understood that all dosages can be continuously given or divided into dosages given per a given timeframe. Examples of timeframes include but are not limited to every 1 hour, 2 hour, 4 hour, 6 hour, 8 hour, 12 hour, 24 hour, 48 hour, or 72 hour, or every week, 2 weeks, 4 weeks, or every month, 2 months, 4 months, and so forth. As used herein, the term "significantly above the optimal range" means, e.g., about 1% to about 50%, about 5% to about 50%, about 10% to about 50%, about 20% to about 50%, about 30% to about 50%, or about 40% to 50% over the optimal range.

The dosage for inhibitors of NELL peptides varies according to the type of the inhibitor, the bone or cartilage condition to be treated, prevented, or ameliorated, and the age, the location, and the gender of the mammalian subject receiving the composition containing the inhibitor. Generally, the dosage for inhibitors of NELL peptides ranges from but at not limited to: 0.001 pg/mm<sup>2</sup> to 1 pg/mm<sup>2</sup>, or more preferably from 0.001 ng/mm<sup>2</sup> to 1 ng/mm<sup>2</sup>, or more preferably from 0.001 μg/mm<sup>2</sup> to 1 μg/mm<sup>2</sup>, or more preferably from 0.001 mg/mm<sup>2</sup> to 1 mg/mm<sup>2</sup>, or more preferably from 0.001 g/mm<sup>2</sup> to 1 g/mm<sup>2</sup>, with or without a particular carrier or scaffold. In another embodiment, the dosage for inhibitors of NELL peptides generally ranges from 0.001 pg/ml to 1 pg/ml, or more preferably from 0.001 ng/ml to 1 ng/ml, or more preferably from 0.001 μg/ml to 1 μg/ml, or more preferably from 0.001 mg/ml to 1 mg/ml, or more preferably from 0.001 g/ml to 100 g/ml, with or without a particular carrier or scaffold. In yet another embodiment, the dosage for inhibitors of NELL peptides generally ranges from 0.001 pg/kg to 1 pg/kg, or more preferably from 0.001 ng/kg to 1 ng/kg, or more preferably from 0.001 μg/kg to 1 μg/kg, or more preferably from 0.001 mg/kg to 1 mg/kg, or more preferably from 0.001 gm/kg to 1 gm/kg, more preferably from 0.001 kg/kg to 1 kg/kg with or without a particular carrier or scaffold. Furthermore, it is understood that all dosages can be continuously given or divided into dosages given per a given timeframe. Examples of timeframes include but are not limited to every 1 hour, 2

hour, 4 hour, 6 hour, 8 hour, 12 hour, 24 hour, 48 hour, or 72 hour, or every week, 2 weeks, 4 weeks, or every month, 2 months, 4 months, and so forth.

The dosage for modulators of receptors of NELL peptides varies according to the type of the inhibitor, the type of receptor, the bone or cartilage condition to be treated, prevented, or ameliorated, and the age, the location, and the gender of the mammalian subject receiving the composition containing the modulators of receptors of NELL peptides. Generally, the dosage for modulators of receptors of NELL peptides ranges from but at not limited to: 0.001 pg/mm<sup>2</sup> to 1 pg/mm<sup>2</sup>, or more preferably from 0.001 ng/mm<sup>2</sup> to 1 ng/mm<sup>2</sup>, or more preferably from 0.001 μg/mm<sup>2</sup> to 1 μg/mm<sup>2</sup>, or more preferably from 0.001 mg/mm<sup>2</sup> to 1 mg/mm<sup>2</sup>, or more preferably from 0.001 g/mm<sup>2</sup> to 1 g/mm<sup>2</sup>, with or without a particular carrier or scaffold. In another embodiment, the dosage for modulators of receptors of NELL peptides generally ranges from 0.001 pg/ml to 1 pg/ml, or more preferably from 0.001 ng/ml to 1 ng/ml, or more preferably from 0.001 μg/ml to 1 μg/ml, or more preferably from 0.001 mg/ml to 1 mg/ml, or more preferably from 0.001 g/ml to 100 g/ml, with or without a particular carrier or scaffold. In yet another embodiment, the dosage for modulators of receptors of NELL peptides generally ranges from 0.001 pg/kg to 1 pg/kg, or more preferably from 0.001 ng/kg to 1 ng/kg, or more preferably from 0.001 μg/kg to 1 μg/kg, or more preferably from 0.001 mg/kg to 1 mg/kg, or more preferably from 0.001 gm/kg to 1 gm/kg, more preferably from 0.001 kg/kg to 1 kg/kg with or without a particular carrier or scaffold. Furthermore, it is understood that all dosages can be continuously given or divided into dosages given per a given timeframe. Examples of timeframes include but are not limited to every 1 hour, 2 hour, 4 hour, 6 hour, 8 hour, 12 hour, 24 hour, 48 hour, or 72 hour, or every week, 2 weeks, 4 weeks, or every month, 2 months, 4 months, and so forth.

#### Dosage Form

The therapeutically effective dose of an agent included in the dosage form can be selected by considering the type of agent selected and the route of administration. The dosage form can include a agent in combination with other inert ingredients, including adjuvants and pharmaceutically acceptable carriers for the facilitation of dosage to the patient, as is known to those skilled in the pharmaceutical arts.

In one embodiment, the invention can include a method of treating a patient to induce cartilage formation, comprising administering NELL1 peptide at a therapeutically effective dose in an effective dosage form at a selected interval to enhance cartilage formation or repair. The method of can further comprise administering at least one secondary agent in the region where cartilage formation or repair is desired, including but not limited to TGF-beta, BMP2, BMP4, BMP7, bFGF, VEGF, PDGF, collagen, bone, bone matrix, tendon matrix or ligament matrix, chondrogenic or osteoblastic cells.

In one embodiment, a method of treating a patient to induce cartilage formation or repair can include harvesting mammalian chondrogenic cells, increasing the concentration of expression of NELL1 peptide in contact with the chondrogenic cells and administering the chondrogenic cells to a region where cartilage formation or repair is desired.

## EXAMPLES

The following examples are offered to illustrate, but not to limit the claimed invention.

## Example 1

## Injectable Devices

An injectable device containing NELL (with or without cells) can be directly injected into spinal discs to promote cartilage formation. A disc nucleus replacement device impregnated with NELL is designed to replace the inner portion of the vertebral disc (the nucleus) or both the inner and outer portion of the disc. An injectable device containing NELL (with or without cells) can be directly injected into the various joint spaces (e.g., knee, temporomandibular joint, wrist) or implanted arthroscopically or openly into various joint spaces.

## Example 2

## Cartilage Differentiation, Maturation and Hypertrophy without Necessarily Mineralization

NELL1 transgenic overexpression mice were created with the rationale was that NELL1 overexpression transgenic mice would exhibit altered intramembranous or endochondral bone formation. The invention was tested with F2 progeny from NELL1 transgenic mice. Histology from various forms of NELL1 overexpression mice has demonstrated increased cartilage differentiation, maturation, and hypertrophy without necessarily mineralization in both hyaline cartilage areas (FIG. 1) and fibrocartilage areas (FIGS. 2A-2F).

Goat auricular cartilage was minced to 1×3 mm pieces and digested with 0.25% trypsin/1 mM EDTA at room temperature for 30 min, followed by 3 mg/ml collagenase II (Sigma, St Louis, Mo., USA) digestion with shaking at 37 C for 6 h. The cell suspension was filtered through a 70 mm strainer and the chondrocytes were then pelleted by centrifugation. After washing with PBS, the cells were cultured in DMEM (Gibco BRL, Grand Island, N.Y., USA) plus 10% fetal calf serum (Hyclone, Logan, Utah, USA), 100 U/ml penicillin and 100 mg/l streptomycin at 37° C. with 5% CO<sub>2</sub>. The cells were then treated/transduced with AdNELL1, AdBMP2, or AdLacZ. The in vitro transduction efficiency was assessed by staining for beta galactosidase (FIG. 3). The cells were combined with pluronic F127 (Sigma) as a common carrier for

nude mice subcutaneous injection/or implantation and then examined at 2 weeks (FIG. 6) or 4 weeks (FIGS. 4, 5, 7-9). A total of 8 million cells were injected/implanted per site.

High-resolution micro-computed tomography (microCT), which utilized 9-20 μm resolution technology from μCT40 (Scanco Medical, Basserdorf, Switzerland) was performed on 4 week samples (FIG. 5). MicroCT data were collected at 55 kVp and 145 μA and reconstructed using the cone-beam algorithm supplied with the microCT scanner by Scanco. Visualization and reconstruction of the data were performed using the μCT Ray T3.3 and μCT Evaluation Program V5.0 provided by Scanco Medical.

Harvested samples were processed and embedded in paraffin wax. Six micron-thick sections, using a microtome (McBain Instruments, Chatsworth, Calif.), were placed on poly-L-lysine-coated Polysine microscope slides (Erie Scientific Company, Portsmouth, N.H.) and baked at 37° C. overnight. Samples were hematoxylin and eosin (H&E) stained. Additional analysis utilized alcian blue staining. Sections were stained with alcian blue solution for 30 min followed by washing in 3% glacial acetic acid followed by water. Sections were then counterstained with nuclear fast red solution and rinsed in distilled water. Finally, sections were dehydrated in alcohol and cleared in xylenes before mounting in permount (FIGS. 6 and 7).

Six-micron-thick sections were dewaxed in xylenes and rehydrated in ethanol baths. Sections were enzyme-treated for antigen retrieval with 20 μg/ml Proteinase K at 37° C. for 10 min and then blocked with 5% horse serum for 2 h at room temperature. Sections were incubated with appropriate primary antibodies at 4° C. overnight then incubated with a biotinylated anti-rabbit IgG secondary antibody (Vector Laboratories, Burlingame, Calif.) for 1 h at room temperature. Positive immunoreactivity was detected using Vectastain ABC reagents and AEC chromagen (both from Vector Laboratories) according to the manufacturer's instructions. Controls for each antibody consisted of incubation with secondary antibody in the absence of primary antibody. Sections were counterstained with hematoxylin for 2 min followed by 10 min in running water. Aqueous mounting medium was used with cover slips.

While particular embodiments of the present invention have been shown and described, it will be obvious to those skilled in the art that changes and modifications can be made without departing from this invention in its broader aspects. Therefore, the appended claims are to encompass within their scope all such changes and modifications as fall within the true spirit and scope of this invention.

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Ser Cys Ile Asp Ile Asp Glu Cys Ala Leu Arg Thr His Thr Cys Trp

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595					600					605					
Asn	Asp	Ser	Ala	Cys	Ile	Asn	Leu	Ala	Gly	Gly	Phe	Asp	Cys	Leu	Cys
610						615					620				
Pro	Ser	Gly	Pro	Ser	Cys	Ser	Gly	Asp	Cys	Pro	His	Glu	Gly	Gly	Leu
625					630					635					640
Lys	His	Asn	Gly	Gln	Val	Trp	Thr	Leu	Lys	Glu	Asp	Arg	Cys	Ser	Val
				645						650					655
Cys	Ser	Cys	Lys	Asp	Gly	Lys	Ile	Phe	Cys	Arg	Arg	Thr	Ala	Cys	Asp
			660					665						670	
Cys	Gln	Asn	Pro	Ser	Ala	Asp	Leu	Phe	Cys	Cys	Pro	Glu	Cys	Asp	Thr
		675					680							685	
Arg	Val	Thr	Ser	Gln	Cys	Leu	Asp	Gln	Asn	Gly	His	Lys	Leu	Tyr	Arg
	690					695					700				
Ser	Gly	Asp	Asn	Trp	Thr	His	Ser	Cys	Gln	Gln	Cys	Arg	Cys	Leu	Glu
705					710					715					720
Gly	Glu	Val	Asp	Cys	Trp	Pro	Leu	Thr	Cys	Pro	Asn	Leu	Ser	Cys	Glu
				725					730						735
Tyr	Thr	Ala	Ile	Leu	Glu	Gly	Glu	Cys	Cys	Pro	Arg	Cys	Val	Ser	Asp
			740					745						750	
Pro	Cys	Leu	Ala	Asp	Asn	Ile	Thr	Tyr	Asp	Ile	Arg	Lys	Thr	Cys	Leu
		755					760					765			
Asp	Ser	Tyr	Gly	Val	Ser	Arg	Leu	Ser	Gly	Ser	Val	Trp	Thr	Met	Ala
		770				775						780			
Gly	Ser	Pro	Cys	Thr	Thr	Cys	Lys	Cys	Lys	Asn	Gly	Arg	Val	Cys	Cys
785					790					795					800
Ser	Val	Asp	Phe	Glu	Cys	Leu	Gln	Asn	Asn						
			805						810						

<210> SEQ ID NO 3  
 <211> LENGTH: 2433  
 <212> TYPE: DNA  
 <213> ORGANISM: Rattus norvegicus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)...(2433)

<400> SEQUENCE: 3

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Met	Pro	Met	Asp	Val	Ile	Leu	Val	Leu	Trp	Phe	Cys	Val	Cys	Thr	Ala	
1				5					10					15		
agg	aca	gtg	ttg	ggc	ttt	ggg	atg	gac	cct	gac	ctt	cag	ctg	gac	atc	96
Arg	Thr	Val	Leu	Gly	Phe	Gly	Met	Asp	Pro	Asp	Leu	Gln	Leu	Asp	Ile	
			20					25					30			
atc	tca	gag	ctc	gac	ctg	gtg	aac	acc	acc	ctg	gga	gtc	acg	cag	gtg	144
Ile	Ser	Glu	Leu	Asp	Leu	Val	Asn	Thr	Thr	Leu	Gly	Val	Thr	Gln	Val	
			35				40					45				
gct	gga	ctg	cac	aac	gcc	agt	aaa	gca	ttt	cta	ttt	caa	gat	gta	cag	192
Ala	Gly	Leu	His	Asn	Ala	Ser	Lys	Ala	Phe	Leu	Phe	Gln	Asp	Val	Gln	
			50				55					60				
aga	gag	atc	cat	tcg	gcc	cct	cac	gtg	agt	gag	aag	ctg	atc	cag	cta	240
Arg	Glu	Ile	His	Ser	Ala	Pro	His	Val	Ser	Glu	Lys	Leu	Ile	Gln	Leu	
	65				70					75					80	
ttc	cgg	aat	aag	agc	gag	ttc	acc	ttt	ttg	gct	aca	gtg	cag	cag	aaa	288
Phe	Arg	Asn	Lys	Ser	Glu	Phe	Thr	Phe	Leu	Ala	Thr	Val	Gln	Gln	Lys	
				85					90					95		
cca	tcc	acc	tca	ggg	gtg	ata	ctg	tcc	atc	cgg	gag	ctg	gag	cac	agc	336
Pro	Ser	Thr	Ser	Gly	Val	Ile	Leu	Ser	Ile	Arg	Glu	Leu	Glu	His	Ser	
			100					105						110		



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tat ttt gaa ctg gag agc agt ggc cca aga gaa gag ata cgc tac cat	384
Tyr Phe Glu Leu Glu Ser Ser Gly Pro Arg Glu Glu Ile Arg Tyr His	
115 120 125	
tac ata cat ggt gga aag ccc agg act gag gcc ctt ccc tac cgc atg	432
Tyr Ile His Gly Gly Lys Pro Arg Thr Glu Ala Leu Pro Tyr Arg Met	
130 135 140	
gca gac gga caa tgg cac aag gtc gcg ctg tca gtg agc gcc tct cac	480
Ala Asp Gly Gln Trp His Lys Val Ala Leu Ser Val Ser Ala Ser His	
145 150 155 160	
ctc ctg ctc cac atc gac tgc aat agg att tac gag cgt gtg ata gac	528
Leu Leu Leu His Ile Asp Cys Asn Arg Ile Tyr Glu Arg Val Ile Asp	
165 170 175	
cct ccg gag acc aac ctt cct cca gga agc aat ctg tgg ctt ggg caa	576
Pro Pro Glu Thr Asn Leu Pro Pro Gly Ser Asn Leu Trp Leu Gly Gln	
180 185 190	
cgt aac caa aag cat ggc ttt ttc aaa gga atc atc caa gat ggt aag	624
Arg Asn Gln Lys His Gly Phe Phe Lys Gly Ile Ile Gln Asp Gly Lys	
195 200 205	
atc atc ttc atg ccg aat ggt ttc atc aca cag tgt ccc aac ctc aat	672
Ile Ile Phe Met Pro Asn Gly Phe Ile Thr Gln Cys Pro Asn Leu Asn	
210 215 220	
cgc act tgc cca aca tgc agt gac ttc ctg agc ctg gtt caa gga ata	720
Arg Thr Cys Pro Thr Cys Ser Asp Phe Leu Ser Leu Val Gln Gly Ile	
225 230 235 240	
atg gat ttg caa gag ctt ttg gcc aag atg act gca aaa ctg aat tat	768
Met Asp Leu Gln Glu Leu Leu Ala Lys Met Thr Ala Lys Leu Asn Tyr	
245 250 255	
gca gag acg aga ctt ggt caa ctg gaa aat tgc cac tgt gag aag acc	816
Ala Glu Thr Arg Leu Gly Gln Leu Glu Asn Cys His Cys Glu Lys Thr	
260 265 270	
tgc caa gtg agt ggg ctg ctc tac agg gac caa gac tcc tgg gtg gat	864
Cys Gln Val Ser Gly Leu Leu Tyr Arg Asp Gln Asp Ser Trp Val Asp	
275 280 285	
ggt gac aac tgt ggg aac tgc acg tgc aaa agt ggt gcc gtg gag tgc	912
Gly Asp Asn Cys Gly Asn Cys Thr Cys Lys Ser Gly Ala Val Glu Cys	
290 295 300	
cgc agg atg tcc tgt ccc ccg ctc aac tgt tcc ccg gac tca ctt cct	960
Arg Arg Met Ser Cys Pro Pro Leu Asn Cys Ser Pro Asp Ser Leu Pro	
305 310 315 320	
gtg cac att tcc ggc cag tgt tgt aaa gtt tgc aga cca aaa tgt atc	1008
Val His Ile Ser Gly Gln Cys Cys Lys Val Cys Arg Pro Lys Cys Ile	
325 330 335	
tat gga gga aaa gtt ctt gct gag ggc cag cgg att tta acc aag acc	1056
Tyr Gly Gly Lys Val Leu Ala Glu Gly Gln Arg Ile Leu Thr Lys Thr	
340 345 350	
tgc cgg gaa tgt cga ggt gga gtc ttg gta aaa atc aca gaa gct tgc	1104
Cys Arg Glu Cys Arg Gly Gly Val Leu Val Lys Ile Thr Glu Ala Cys	
355 360 365	
cct cct ttg aac tgc tca gca aag gat cat att ctt cca gag aat cag	1152
Pro Pro Leu Asn Cys Ser Ala Lys Asp His Ile Leu Pro Glu Asn Gln	
370 375 380	
tgc tgc agg gtc tgc cca ggt cat aac ttc tgt gca gaa gca cct aag	1200
Cys Cys Arg Val Cys Pro Gly His Asn Phe Cys Ala Glu Ala Pro Lys	
385 390 395 400	
tgc gga gaa aac tcg gaa tgc aaa aat tgg aat aca aaa gca acc tgt	1248
Cys Gly Glu Asn Ser Glu Cys Lys Asn Trp Asn Thr Lys Ala Thr Cys	
405 410 415	
gag tgc aag aat gga tac atc tct gtc cag ggc aac tct gca tac tgt	1296
Glu Cys Lys Asn Gly Tyr Ile Ser Val Gln Gly Asn Ser Ala Tyr Cys	
420 425 430	

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gaa gat att gat gag tgt gca gct aaa atg cac tat tgt cat gcc aac	1344
Glu Asp Ile Asp Glu Cys Ala Ala Lys Met His Tyr Cys His Ala Asn	
435 440 445	
acc gtg tgt gtc aac ttg ccg ggg ttg tat cgc tgt gac tgc gtc cca	1392
Thr Val Cys Val Asn Leu Pro Gly Leu Tyr Arg Cys Asp Cys Val Pro	
450 455 460	
ggg tac atc cgt gtg gat gac ttc tct tgt acg gag cat gat gat tgt	1440
Gly Tyr Ile Arg Val Asp Asp Phe Ser Cys Thr Glu His Asp Asp Cys	
465 470 475 480	
ggc agc gga caa cac aac tgc gac aaa aat gcc atc tgt acc aac aca	1488
Gly Ser Gly Gln His Asn Cys Asp Lys Asn Ala Ile Cys Thr Asn Thr	
485 490 495	
gtc cag gga cac agc tgc acc tgc cag ccg ggt tac gtg gga aat ggc	1536
Val Gln Gly His Ser Cys Thr Cys Gln Pro Gly Tyr Val Gly Asn Gly	
500 505 510	
acc atc tgc aaa gca ttc tgt gaa gag ggt tgc aga tac gga ggt acc	1584
Thr Ile Cys Lys Ala Phe Cys Glu Glu Gly Cys Arg Tyr Gly Gly Thr	
515 520 525	
tgt gtg gct cct aac aag tgt gtc tgt cct tct gga ttc acg gga agc	1632
Cys Val Ala Pro Asn Lys Cys Val Cys Pro Ser Gly Phe Thr Gly Ser	
530 535 540	
cac tgt gag aaa gat att gat gaa tgc gca gag gga ttc gtt gaa tgc	1680
His Cys Glu Lys Asp Ile Asp Glu Cys Ala Glu Gly Phe Val Glu Cys	
545 550 555 560	
cac aac tac tcc cgc tgt gtt aac ctg cca ggg tgg tac cac tgt gag	1728
His Asn Tyr Ser Arg Cys Val Asn Leu Pro Gly Trp Tyr His Cys Glu	
565 570 575	
tgc aga agc ggt ttc cat gac gat ggg acc tac tca ctg tcc ggg gag	1776
Cys Arg Ser Gly Phe His Asp Asp Gly Thr Tyr Ser Leu Ser Gly Glu	
580 585 590	
tcc tgc att gat atc gat gaa tgt gcc tta aga act cac act tgt tgg	1824
Ser Cys Ile Asp Ile Asp Glu Cys Ala Leu Arg Thr His Thr Cys Trp	
595 600 605	
aat gac tct gcc tgc atc aac tta gca gga gga ttt gac tgc ctg tgt	1872
Asn Asp Ser Ala Cys Ile Asn Leu Ala Gly Gly Phe Asp Cys Leu Cys	
610 615 620	
ccc tct ggg ccc tcc tgc tct ggt gac tgt ccc cac gaa gga ggg ctg	1920
Pro Ser Gly Pro Ser Cys Ser Gly Asp Cys Pro His Glu Gly Gly Leu	
625 630 635 640	
aag cat aat ggg cag gtg tgg att ctg aga gaa gac agg tgt tca gtc	1968
Lys His Asn Gly Gln Val Trp Ile Leu Arg Glu Asp Arg Cys Ser Val	
645 650 655	
tgt tcc tgc aag gat ggg aag ata ttc tgc cgg cgg aca gct tgt gat	2016
Cys Ser Cys Lys Asp Gly Lys Ile Phe Cys Arg Arg Thr Ala Cys Asp	
660 665 670	
tgc cag aat cca aat gtt gac ctt ttt tgc tgc cca gag tgc gat acc	2064
Cys Gln Asn Pro Asn Val Asp Leu Phe Cys Cys Pro Glu Cys Asp Thr	
675 680 685	
agg gtc acc agc caa tgt tta gat caa agt gga cag aag ctc tat cga	2112
Arg Val Thr Ser Gln Cys Leu Asp Gln Ser Gly Gln Lys Leu Tyr Arg	
690 695 700	
agt gga gac aac tgg acc cac agc tgc cag cag tgc cga tgt ctg gaa	2160
Ser Gly Asp Asn Trp Thr His Ser Cys Gln Gln Cys Arg Cys Leu Glu	
705 710 715 720	
gga gag gca gac tgc tgg cct ctg gct tgc cct agt ttg ggc tgt gaa	2208
Gly Glu Ala Asp Cys Trp Pro Leu Ala Cys Pro Ser Leu Gly Cys Glu	
725 730 735	
tac aca gcc atg ttt gaa ggg gag tgt tgt ccc cga tgt gtc agt gac	2256
Tyr Thr Ala Met Phe Glu Gly Glu Cys Cys Pro Arg Cys Val Ser Asp	
740 745 750	

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ccc tgc ctg gct ggt aat att gcc tat gac atc aga aaa act tgc ctg      2304
Pro Cys Leu Ala Gly Asn Ile Ala Tyr Asp Ile Arg Lys Thr Cys Leu
      755                      760                      765

gac agc ttt ggt gtt tcg agg ctg agc gga gcc gtg tgg aca atg gct      2352
Asp Ser Phe Gly Val Ser Arg Leu Ser Gly Ala Val Trp Thr Met Ala
      770                      775                      780

gga tct cct tgt aca acc tgc aaa tgc aag aat ggg aga gtc tgc tgc      2400
Gly Ser Pro Cys Thr Thr Cys Lys Cys Lys Asn Gly Arg Val Cys Cys
      785                      790                      795                      800

tct gtg gat ctg gag tgt att gag aat aac tga      2433
Ser Val Asp Leu Glu Cys Ile Glu Asn Asn *
      805                      810

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<210> SEQ ID NO 4
<211> LENGTH: 810
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

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<400> SEQUENCE: 4

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Met Pro Met Asp Val Ile Leu Val Leu Trp Phe Cys Val Cys Thr Ala
  1                    5                    10                    15

Arg Thr Val Leu Gly Phe Gly Met Asp Pro Asp Leu Gln Leu Asp Ile
      20                    25                    30

Ile Ser Glu Leu Asp Leu Val Asn Thr Thr Leu Gly Val Thr Gln Val
      35                    40                    45

Ala Gly Leu His Asn Ala Ser Lys Ala Phe Leu Phe Gln Asp Val Gln
      50                    55                    60

Arg Glu Ile His Ser Ala Pro His Val Ser Glu Lys Leu Ile Gln Leu
      65                    70                    75                    80

Phe Arg Asn Lys Ser Glu Phe Thr Phe Leu Ala Thr Val Gln Gln Lys
      85                    90                    95

Pro Ser Thr Ser Gly Val Ile Leu Ser Ile Arg Glu Leu Glu His Ser
      100                   105                   110

Tyr Phe Glu Leu Glu Ser Ser Gly Pro Arg Glu Glu Ile Arg Tyr His
      115                   120                   125

Tyr Ile His Gly Gly Lys Pro Arg Thr Glu Ala Leu Pro Tyr Arg Met
      130                   135                   140

Ala Asp Gly Gln Trp His Lys Val Ala Leu Ser Val Ser Ala Ser His
      145                   150                   155                   160

Leu Leu Leu His Ile Asp Cys Asn Arg Ile Tyr Glu Arg Val Ile Asp
      165                   170                   175

Pro Pro Glu Thr Asn Leu Pro Pro Gly Ser Asn Leu Trp Leu Gly Gln
      180                   185                   190

Arg Asn Gln Lys His Gly Phe Phe Lys Gly Ile Ile Gln Asp Gly Lys
      195                   200                   205

Ile Ile Phe Met Pro Asn Gly Phe Ile Thr Gln Cys Pro Asn Leu Asn
      210                   215                   220

Arg Thr Cys Pro Thr Cys Ser Asp Phe Leu Ser Leu Val Gln Gly Ile
      225                   230                   235                   240

Met Asp Leu Gln Glu Leu Leu Ala Lys Met Thr Ala Lys Leu Asn Tyr
      245                   250                   255

Ala Glu Thr Arg Leu Gly Gln Leu Glu Asn Cys His Cys Glu Lys Thr
      260                   265                   270

Cys Gln Val Ser Gly Leu Leu Tyr Arg Asp Gln Asp Ser Trp Val Asp
      275                   280                   285

Gly Asp Asn Cys Gly Asn Cys Thr Cys Lys Ser Gly Ala Val Glu Cys
      290                   295                   300

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Arg Arg Met Ser Cys Pro Pro Leu Asn Cys Ser Pro Asp Ser Leu Pro  
 305 310 315 320  
 Val His Ile Ser Gly Gln Cys Cys Lys Val Cys Arg Pro Lys Cys Ile  
 325 330 335  
 Tyr Gly Gly Lys Val Leu Ala Glu Gly Gln Arg Ile Leu Thr Lys Thr  
 340 345 350  
 Cys Arg Glu Cys Arg Gly Gly Val Leu Val Lys Ile Thr Glu Ala Cys  
 355 360 365  
 Pro Pro Leu Asn Cys Ser Ala Lys Asp His Ile Leu Pro Glu Asn Gln  
 370 375 380  
 Cys Cys Arg Val Cys Pro Gly His Asn Phe Cys Ala Glu Ala Pro Lys  
 385 390 395 400  
 Cys Gly Glu Asn Ser Glu Cys Lys Asn Trp Asn Thr Lys Ala Thr Cys  
 405 410 415  
 Glu Cys Lys Asn Gly Tyr Ile Ser Val Gln Gly Asn Ser Ala Tyr Cys  
 420 425 430  
 Glu Asp Ile Asp Glu Cys Ala Ala Lys Met His Tyr Cys His Ala Asn  
 435 440 445  
 Thr Val Cys Val Asn Leu Pro Gly Leu Tyr Arg Cys Asp Cys Val Pro  
 450 455 460  
 Gly Tyr Ile Arg Val Asp Asp Phe Ser Cys Thr Glu His Asp Asp Cys  
 465 470 475 480  
 Gly Ser Gly Gln His Asn Cys Asp Lys Asn Ala Ile Cys Thr Asn Thr  
 485 490 495  
 Val Gln Gly His Ser Cys Thr Cys Gln Pro Gly Tyr Val Gly Asn Gly  
 500 505 510  
 Thr Ile Cys Lys Ala Phe Cys Glu Glu Gly Cys Arg Tyr Gly Gly Thr  
 515 520 525  
 Cys Val Ala Pro Asn Lys Cys Val Cys Pro Ser Gly Phe Thr Gly Ser  
 530 535 540  
 His Cys Glu Lys Asp Ile Asp Glu Cys Ala Glu Gly Phe Val Glu Cys  
 545 550 555 560  
 His Asn Tyr Ser Arg Cys Val Asn Leu Pro Gly Trp Tyr His Cys Glu  
 565 570 575  
 Cys Arg Ser Gly Phe His Asp Asp Gly Thr Tyr Ser Leu Ser Gly Glu  
 580 585 590  
 Ser Cys Ile Asp Ile Asp Glu Cys Ala Leu Arg Thr His Thr Cys Trp  
 595 600 605  
 Asn Asp Ser Ala Cys Ile Asn Leu Ala Gly Gly Phe Asp Cys Leu Cys  
 610 615 620  
 Pro Ser Gly Pro Ser Cys Ser Gly Asp Cys Pro His Glu Gly Gly Leu  
 625 630 635 640  
 Lys His Asn Gly Gln Val Trp Ile Leu Arg Glu Asp Arg Cys Ser Val  
 645 650 655  
 Cys Ser Cys Lys Asp Gly Lys Ile Phe Cys Arg Arg Thr Ala Cys Asp  
 660 665 670  
 Cys Gln Asn Pro Asn Val Asp Leu Phe Cys Cys Pro Glu Cys Asp Thr  
 675 680 685  
 Arg Val Thr Ser Gln Cys Leu Asp Gln Ser Gly Gln Lys Leu Tyr Arg  
 690 695 700  
 Ser Gly Asp Asn Trp Thr His Ser Cys Gln Gln Cys Arg Cys Leu Glu  
 705 710 715 720  
 Gly Glu Ala Asp Cys Trp Pro Leu Ala Cys Pro Ser Leu Gly Cys Glu

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	725		730		735
Tyr Thr Ala Met Phe Glu Gly Glu Cys Cys Pro Arg Cys Val Ser Asp					
	740		745		750
Pro Cys Leu Ala Gly Asn Ile Ala Tyr Asp Ile Arg Lys Thr Cys Leu					
	755		760		765
Asp Ser Phe Gly Val Ser Arg Leu Ser Gly Ala Val Trp Thr Met Ala					
	770		775		780
Gly Ser Pro Cys Thr Thr Cys Lys Cys Lys Asn Gly Arg Val Cys Cys					
	785		790		800
Ser Val Asp Leu Glu Cys Ile Glu Asn Asn					
	805		810		

&lt;210&gt; SEQ ID NO 5

&lt;211&gt; LENGTH: 2433

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mus musculus

&lt;400&gt; SEQUENCE: 5

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ggctttggga tggaccctga ccttcagatg gacatcatca ctgaacttga ccttgtgaac    120
accaccctgg gcgtcactca ggtggctgga ctacacaatg ccagtaaggc atttctgttt    180
caagatgtac agagagagat ccaactcagcc cctcatgtga gtgagaagct gatccagcta    240
ttccggaata agagtgagtt tacctttttg gctacagtgc agcagaagcc gtccacctca    300
ggggtgatac tgtcgatccg ggagctggaa cacagctatt ttgaactgga gagcagtggc    360
ccaagagaag agatacgtta tcattacatc catggcggca agcccaggac tgaggccctt    420
ccctaccgca tggccgatgg acagtggcac aaggctcgcg tgtctgtgag cgcctctcac    480
ctcctactcc atgtcgactg caataggatt tatgagcgtg tgatagatcc tccggagacc    540
aaccttctc caggaagcaa tctatggctt gggcaacgta atcaaaagca tggctttttc    600
aaaggaatca tccaagatgg caagatcatc ttcatgccga acggcttcat cacacagtgc    660
cccaacctaa atcgcaactg cccaacatgc agtgatttcc tgagcctggt tcaaggaata    720
atggatttgc aagagctttt ggccaagatg actgcaaaac tgaattatgc agagacgaga    780
cttggtaaac tggaaaattg ccaactgtgag aagacctgcc aagtgagtgg gctgctctac    840
agggaccaag actcctgggt agatggtgac aactgcagga actgcacatg caaaagtggg    900
gctgtggagt gccgaaggat gtctgtccc ccaactcaact gttccccaga ctcacttctc    960
gtgcatatth ctggccaatg ttgtaaagtt tgcagaccaa aatgtatcta tggaggaaaa   1020
gttcttgctg agggccagcg gattttaacc aagacctgcc gggaatgtcg aggtggagtc   1080
ttggtaaaaa tcacagaagc ttgccctcct ttgaactgct cagagaagga tcatattctt   1140
ccggagaacc agtgetgcag ggtctgccga ggtcataact tctgtgcaga agcacctaag   1200
tgtggagaaa actcggaatg caaaaattgg aatacaaaag cgacttgtga gtgcaagaat   1260
ggatacatct ctgtccaggg caactctgca tactgtgaag atatcgatga gtgtgcagca   1320
aagatgcact actgtcatgc caacacggtg tgtgtcaact tgccgggggt atatcgctgt   1380
gactgcatcc caggatacat ccgtgtggat gacttctctt gtacggagca tgatgattgt   1440
ggcagcggac aacacaactg tgacaaaaat gccatctgta ccaacacagt ccagggacac   1500
agctgtacct gccagccagg ctacgtggga aatggtactg tctgcaaagc attctgtgaa   1560
gagggttgca gatacggagg tacctgtgtg gccctaaca aatgtgtctg tcttctgga   1620
ttcacaggaa gccactgtga gaaagatatt gatgaatgtg cagagggatt cgttgagtgc   1680

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cacaaccact cccgctgcgt taaccttcca ggggtgtacc actgtgagtg cagaagcggg 1740
ttccatgacg atgggacctt ttcactgtcc ggggagtcct gcattgatat tgatgaatgt 1800
gccttaagaa ctcacacttg ttggaatgac tctgcctgca tcaacttagc aggaggattt 1860
gactgcctgt gtcctctggt gccctcctgc tctggtgact gtccccacga aggggggctg 1920
aagcataatg ggcaggtgtg gattctgaga gaagacaggt gttcagtcctg ttctgtgaag 1980
gatgggaaga tattctgccc ggggacagct tgtgattgcc agaatccaaa tgttgacctt 2040
ttctgctgcc cagagtgtga caccaggggc actagccaat gtttagatca aagcggacag 2100
aagctctatc gaagtggaga caactggacc cacagctgcc agcagtgccc atgtctggaa 2160
ggagaggcag actgctggcc tctagcttgc cctagtttga gctgtgaata cacagccatc 2220
tttgaaggag agtgttgtcc ccgctgtgtc agtgaccctt gcttggtgta taatattgcc 2280
tatgacatca gaaaaacttg cctggacagc tctggtatct cgaggctgag cggcgcagtg 2340
tggacaatgg ctggatctcc ctgtacaacc tgtcaatgca agaatgggag agtctgctgc 2400
tctgtggatc tgggtgtgtc tgagaataac tga 2433

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&lt;210&gt; SEQ ID NO 6

&lt;211&gt; LENGTH: 810

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Mus musculus

&lt;400&gt; SEQUENCE: 6

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Met Pro Met Asp Val Ile Leu Val Leu Trp Phe Cys Val Cys Thr Ala
 1           5           10          15
Arg Thr Val Leu Gly Phe Gly Met Asp Pro Asp Leu Gln Met Asp Ile
          20          25          30
Ile Thr Glu Leu Asp Leu Val Asn Thr Thr Leu Gly Val Thr Gln Val
          35          40          45
Ala Gly Leu His Asn Ala Ser Lys Ala Phe Leu Phe Gln Asp Val Gln
          50          55          60
Arg Glu Ile His Ser Ala Pro His Val Ser Glu Lys Leu Ile Gln Leu
          65          70          75          80
Phe Arg Asn Lys Ser Glu Phe Thr Phe Leu Ala Thr Val Gln Gln Lys
          85          90          95
Pro Ser Thr Ser Gly Val Ile Leu Ser Ile Arg Glu Leu Glu His Ser
          100         105         110
Tyr Phe Glu Leu Glu Ser Ser Gly Pro Arg Glu Glu Ile Arg Tyr His
          115         120         125
Tyr Ile His Gly Gly Lys Pro Arg Thr Glu Ala Leu Pro Tyr Arg Met
          130         135         140
Ala Asp Gly Gln Trp His Lys Val Ala Leu Ser Val Ser Ala Ser His
          145         150         155         160
Leu Leu Leu His Val Asp Cys Asn Arg Ile Tyr Glu Arg Val Ile Asp
          165         170         175
Pro Pro Glu Thr Asn Leu Pro Pro Gly Ser Asn Leu Trp Leu Gly Gln
          180         185         190
Arg Asn Gln Lys His Gly Phe Phe Lys Gly Ile Ile Gln Asp Gly Lys
          195         200         205
Ile Ile Phe Met Pro Asn Gly Phe Ile Thr Gln Cys Pro Asn Leu Asn
          210         215         220
Arg Thr Cys Pro Thr Cys Ser Asp Phe Leu Ser Leu Val Gln Gly Ile
          225         230         235         240

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Met	Asp	Leu	Gln	Glu	Leu	Leu	Ala	Lys	Met	Thr	Ala	Lys	Leu	Asn	Tyr	245	250	255	
Ala	Glu	Thr	Arg	Leu	Gly	Gln	Leu	Glu	Asn	Cys	His	Cys	Glu	Lys	Thr	260	265	270	
Cys	Gln	Val	Ser	Gly	Leu	Leu	Tyr	Arg	Asp	Gln	Asp	Ser	Trp	Val	Asp	275	280	285	
Gly	Asp	Asn	Cys	Arg	Asn	Cys	Thr	Cys	Lys	Ser	Gly	Ala	Val	Glu	Cys	290	295	300	
Arg	Arg	Met	Ser	Cys	Pro	Pro	Leu	Asn	Cys	Ser	Pro	Asp	Ser	Leu	Pro	305	310	315	320
Val	His	Ile	Ser	Gly	Gln	Cys	Cys	Lys	Val	Cys	Arg	Pro	Lys	Cys	Ile	325	330	335	
Tyr	Gly	Gly	Lys	Val	Leu	Ala	Glu	Gly	Gln	Arg	Ile	Leu	Thr	Lys	Thr	340	345	350	
Cys	Arg	Glu	Cys	Arg	Gly	Gly	Val	Leu	Val	Lys	Ile	Thr	Glu	Ala	Cys	355	360	365	
Pro	Pro	Leu	Asn	Cys	Ser	Glu	Lys	Asp	His	Ile	Leu	Pro	Glu	Asn	Gln	370	375	380	
Cys	Cys	Arg	Val	Cys	Arg	Gly	His	Asn	Phe	Cys	Ala	Glu	Ala	Pro	Lys	385	390	395	400
Cys	Gly	Glu	Asn	Ser	Glu	Cys	Lys	Asn	Trp	Asn	Thr	Lys	Ala	Thr	Cys	405	410	415	
Glu	Cys	Lys	Asn	Gly	Tyr	Ile	Ser	Val	Gln	Gly	Asn	Ser	Ala	Tyr	Cys	420	425	430	
Glu	Asp	Ile	Asp	Glu	Cys	Ala	Ala	Lys	Met	His	Tyr	Cys	His	Ala	Asn	435	440	445	
Thr	Val	Cys	Val	Asn	Leu	Pro	Gly	Leu	Tyr	Arg	Cys	Asp	Cys	Ile	Pro	450	455	460	
Gly	Tyr	Ile	Arg	Val	Asp	Asp	Phe	Ser	Cys	Thr	Glu	His	Asp	Asp	Cys	465	470	475	480
Gly	Ser	Gly	Gln	His	Asn	Cys	Asp	Lys	Asn	Ala	Ile	Cys	Thr	Asn	Thr	485	490	495	
Val	Gln	Gly	His	Ser	Cys	Thr	Cys	Gln	Pro	Gly	Tyr	Val	Gly	Asn	Gly	500	505	510	
Thr	Val	Cys	Lys	Ala	Phe	Cys	Glu	Glu	Gly	Cys	Arg	Tyr	Gly	Gly	Thr	515	520	525	
Cys	Val	Ala	Pro	Asn	Lys	Cys	Val	Cys	Pro	Ser	Gly	Phe	Thr	Gly	Ser	530	535	540	
His	Cys	Glu	Lys	Asp	Ile	Asp	Glu	Cys	Ala	Glu	Gly	Phe	Val	Glu	Cys	545	550	555	560
His	Asn	His	Ser	Arg	Cys	Val	Asn	Leu	Pro	Gly	Trp	Tyr	His	Cys	Glu	565	570	575	
Cys	Arg	Ser	Gly	Phe	His	Asp	Asp	Gly	Thr	Tyr	Ser	Leu	Ser	Gly	Glu	580	585	590	
Ser	Cys	Ile	Asp	Ile	Asp	Glu	Cys	Ala	Leu	Arg	Thr	His	Thr	Cys	Trp	595	600	605	
Asn	Asp	Ser	Ala	Cys	Ile	Asn	Leu	Ala	Gly	Gly	Phe	Asp	Cys	Leu	Cys	610	615	620	
Pro	Ser	Gly	Pro	Ser	Cys	Ser	Gly	Asp	Cys	Pro	His	Glu	Gly	Gly	Leu	625	630	635	640
Lys	His	Asn	Gly	Gln	Val	Trp	Ile	Leu	Arg	Glu	Asp	Arg	Cys	Ser	Val	645	650	655	
Cys	Ser	Cys	Lys	Asp	Gly	Lys	Ile	Phe	Cys	Arg	Arg	Thr	Ala	Cys	Asp	660	665	670	

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Cys Gln Asn Pro Asn Val Asp Leu Phe Cys Cys Pro Glu Cys Asp Thr  
675 680 685

Arg Val Thr Ser Gln Cys Leu Asp Gln Ser Gly Gln Lys Leu Tyr Arg  
690 695 700

Ser Gly Asp Asn Trp Thr His Ser Cys Gln Gln Cys Arg Cys Leu Glu  
705 710 715 720

Gly Glu Ala Asp Cys Trp Pro Leu Ala Cys Pro Ser Leu Ser Cys Glu  
725 730 735

Tyr Thr Ala Ile Phe Glu Gly Glu Cys Cys Pro Arg Cys Val Ser Asp  
740 745 750

Pro Cys Leu Ala Asp Asn Ile Ala Tyr Asp Ile Arg Lys Thr Cys Leu  
755 760 765

Asp Ser Ser Gly Ile Ser Arg Leu Ser Gly Ala Val Trp Thr Met Ala  
770 775 780

Gly Ser Pro Cys Thr Thr Cys Gln Cys Lys Asn Gly Arg Val Cys Cys  
785 790 795 800

Ser Val Asp Leu Val Cys Leu Glu Asn Asn  
805 810

<210> SEQ ID NO 7  
<211> LENGTH: 2451  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)...(2451)

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Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu  
1 5 10 15

gga gca gtt tgg ggg ctt ggt gtg gac cct tcc cta cag att gac gtc 96  
Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val  
20 25 30

tta aca gag tta gaa ctt ggg gag tcc acg acc gga gtg cgt cag gtc 144  
Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val  
35 40 45

ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc ttt caa gat act ccc 192  
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro  
50 55 60

aga agc ata aaa gca tcc act gct aca gct gaa cag ttt ttt cag aag 240  
Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys  
65 70 75 80

ctg aga aat aaa cat gaa ttt act att ttg gtg acc cta aaa cag acc 288  
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr  
85 90 95

cac tta aat tca gga gtt att ctc tca att cac cac ttg gat cac agg 336  
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg  
100 105 110

tac ctg gaa ctg gaa agt agt ggc cat cgg aat gaa gtc aga ctg cat 384  
Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Val Arg Leu His  
115 120 125

tac cgc tca ggc agt cac cgc cct cac aca gaa gtg ttt cct tac att 432  
Tyr Arg Ser Gly Ser His Arg Pro His Thr Glu Val Phe Pro Tyr Ile  
130 135 140

ttg gct gat gac aag tgg cac aag ctc tcc tta gcc atc agt gct tcc 480  
Leu Ala Asp Asp Lys Trp His Lys Leu Ser Leu Ala Ile Ser Ala Ser  
145 150 155 160

cat ttg att tta cac att gac tgc aat aaa att tat gaa agg gta gta 528



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His	Leu	Ile	Leu	His	Ile	Asp	Cys	Asn	Lys	Ile	Tyr	Glu	Arg	Val	Val		
				165					170					175			
gaa	aag	ccc	tcc	aca	gac	ttg	cct	cta	ggc	aca	aca	ttt	tgg	cta	gga		576
Glu	Lys	Pro	Ser	Thr	Asp	Leu	Pro	Leu	Gly	Thr	Thr	Phe	Trp	Leu	Gly		
			180					185					190				
cag	aga	aat	aat	gcg	cat	gga	tat	ttt	aag	ggg	ata	atg	caa	gat	gtc		624
Gln	Arg	Asn	Asn	Ala	His	Gly	Tyr	Phe	Lys	Gly	Ile	Met	Gln	Asp	Val		
		195					200					205					
caa	tta	ctt	gtc	atg	ccc	cag	gga	ttt	att	gct	cag	tgc	cca	gat	ctt		672
Gln	Leu	Leu	Val	Met	Pro	Gln	Gly	Phe	Ile	Ala	Gln	Cys	Pro	Asp	Leu		
	210					215					220						
aat	cgc	acc	tgt	cca	act	tgc	aat	gac	ttc	cat	gga	ctt	gtg	cag	aaa		720
Asn	Arg	Thr	Cys	Pro	Thr	Cys	Asn	Asp	Phe	His	Gly	Leu	Val	Gln	Lys		
225					230					235				240			
atc	atg	gag	cta	cag	gat	att	tta	gcc	aaa	aca	tca	gcc	aag	ctg	tct		768
Ile	Met	Glu	Leu	Gln	Asp	Ile	Leu	Ala	Lys	Thr	Ser	Ala	Lys	Leu	Ser		
				245					250					255			
cga	gct	gaa	cag	cga	atg	aat	aga	ttg	gat	cag	tgc	tat	tgt	gaa	agg		816
Arg	Ala	Glu	Gln	Arg	Met	Asn	Arg	Leu	Asp	Gln	Cys	Tyr	Cys	Glu	Arg		
			260					265					270				
act	tgc	acc	atg	aag	gga	acc	acc	tac	cga	gaa	ttt	gag	tcc	tgg	ata		864
Thr	Cys	Thr	Met	Lys	Gly	Thr	Thr	Tyr	Arg	Glu	Phe	Glu	Ser	Trp	Ile		
		275						280				285					
gac	ggc	tgt	aag	aac	tgc	aca	tgc	ctg	aat	gga	acc	atc	cag	tgt	gaa		912
Asp	Gly	Cys	Lys	Asn	Cys	Thr	Cys	Leu	Asn	Gly	Thr	Ile	Gln	Cys	Glu		
	290					295					300						
act	cta	atc	tgc	cca	aat	cct	gac	tgc	cca	ctt	aag	tcg	gct	ctt	gcg		960
Thr	Leu	Ile	Cys	Pro	Asn	Pro	Asp	Cys	Pro	Leu	Lys	Ser	Ala	Leu	Ala		
305					310					315				320			
tat	gtg	gat	ggc	aaa	tgc	tgt	aag	gaa	tgc	aaa	tcg	ata	tgc	caa	ttt		1008
Tyr	Val	Asp	Gly	Lys	Cys	Cys	Lys	Glu	Cys	Lys	Ser	Ile	Cys	Gln	Phe		
				325					330					335			
caa	gga	cga	acc	tac	ttt	gaa	gga	gaa	aga	aat	aca	gtc	tat	tcc	tct		1056
Gln	Gly	Arg	Thr	Tyr	Phe	Glu	Gly	Glu	Arg	Asn	Thr	Val	Tyr	Ser	Ser		
			340					345					350				
tct	gga	gta	tgt	ggt	ctc	tat	gag	tgc	aag	gac	cag	acc	atg	aaa	ctt		1104
Ser	Gly	Val	Cys	Val	Leu	Tyr	Glu	Cys	Lys	Asp	Gln	Thr	Met	Lys	Leu		
		355					360					365					
ggt	gag	agt	tca	ggc	tgt	cca	gct	ttg	gat	tgt	cca	gag	tct	cat	cag		1152
Val	Glu	Ser	Ser	Gly	Cys	Pro	Ala	Leu	Asp	Cys	Pro	Glu	Ser	His	Gln		
	370					375					380						
ata	acc	ttg	tct	cac	agc	tgt	tgc	aaa	ggt	tgt	aaa	ggg	tat	gac	ttt		1200
Ile	Thr	Leu	Ser	His	Ser	Cys	Cys	Lys	Val	Cys	Lys	Gly	Tyr	Asp	Phe		
385					390					395				400			
tgt	tct	gaa	agg	cat	aac	tgc	atg	gag	aat	tcc	atc	tgc	aga	aat	ctg		1248
Cys	Ser	Glu	Arg	His	Asn	Cys	Met	Glu	Asn	Ser	Ile	Cys	Arg	Asn	Leu		
				405					410					415			
aat	gac	agg	gct	ggt	tgt	agc	tgt	cga	gat	ggg	ttt	agg	gct	ctt	cga		1296
Asn	Asp	Arg	Ala	Val	Cys	Ser	Cys	Arg	Asp	Gly	Phe	Arg	Ala	Leu	Arg		
			420					425					430				
gag	gat	aat	gcc	tac	tgt	gaa	gac	atc	gat	gag	tgt	gct	gaa	ggg	cgc		1344
Glu	Asp	Asn	Ala	Tyr	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Ala	Glu	Gly	Arg		
		435					440					445					
cat	tac	tgt	cgt	gaa	aat	aca	atg	tgt	gtc	aac	acc	ccg	ggg	tct	ttt		1392
His	Tyr	Cys	Arg	Glu	Asn	Thr	Met	Cys	Val	Asn	Thr	Pro	Gly	Ser	Phe		
		450				455					460						
atg	tgc	atc	tgc	aaa	act	gga	tac	atc	aga	att	gat	gat	tat	tca	tgt		1440
Met	Cys	Ile	Cys	Lys	Thr	Gly	Tyr	Ile	Arg	Ile	Asp	Asp	Tyr	Ser	Cys		
465					470					475				480			
aca	gaa	cat	gat	gag	tgt	atc	aca	aat	cag	cac	aac	tgt	gat	gaa	aat		1488

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Thr	Glu	His	Asp	Glu	Cys	Ile	Thr	Asn	Gln	His	Asn	Cys	Asp	Glu	Asn	
				485					490					495		
gct	tta	tgc	ttc	aac	act	ggt	gga	gga	cac	aac	tgt	ggt	tgc	aag	ccg	1536
Ala	Leu	Cys	Phe	Asn	Thr	Val	Gly	Gly	His	Asn	Cys	Val	Cys	Lys	Pro	
			500					505					510			
ggc	tat	aca	ggg	aat	gga	acg	aca	tgc	aaa	gca	ttt	tgc	aaa	gat	ggc	1584
Gly	Tyr	Thr	Gly	Asn	Gly	Thr	Thr	Cys	Lys	Ala	Phe	Cys	Lys	Asp	Gly	
		515					520					525				
tgt	agg	aat	gga	gga	gcc	tgt	att	gcc	gct	aat	gtg	tgt	gcc	tgc	cca	1632
Cys	Arg	Asn	Gly	Gly	Ala	Cys	Ile	Ala	Ala	Asn	Val	Cys	Ala	Cys	Pro	
	530					535				540						
caa	ggc	ttc	act	gga	ccc	agc	tgt	gaa	acg	gac	att	gat	gaa	tgc	tct	1680
Gln	Gly	Phe	Thr	Gly	Pro	Ser	Cys	Glu	Thr	Asp	Ile	Asp	Glu	Cys	Ser	
545				550						555					560	
gat	ggt	ttt	ggt	caa	tgt	gac	agt	cgt	gct	aat	tgc	att	aac	ctg	cct	1728
Asp	Gly	Phe	Val	Gln	Cys	Asp	Ser	Arg	Ala	Asn	Cys	Ile	Asn	Leu	Pro	
			565					570						575		
gga	tgg	tac	cac	tgt	gag	tgc	aga	gat	ggc	tac	cat	gac	aat	ggg	atg	1776
Gly	Trp	Tyr	His	Cys	Glu	Cys	Arg	Asp	Gly	Tyr	His	Asp	Asn	Gly	Met	
			580					585					590			
ttt	tca	cca	agt	gga	gaa	tcg	tgt	gaa	gat	att	gat	gag	tgt	ggg	acc	1824
Phe	Ser	Pro	Ser	Gly	Glu	Ser	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gly	Thr	
		595					600					605				
ggg	agg	cac	agc	tgt	gcc	aat	gat	acc	att	tgc	ttc	aat	ttg	gat	ggc	1872
Gly	Arg	His	Ser	Cys	Ala	Asn	Asp	Thr	Ile	Cys	Phe	Asn	Leu	Asp	Gly	
	610					615					620					
gga	tat	gat	tgt	cga	tgt	cct	cat	gga	aag	aat	tgc	aca	ggg	gac	tgc	1920
Gly	Tyr	Asp	Cys	Arg	Cys	Pro	His	Gly	Lys	Asn	Cys	Thr	Gly	Asp	Cys	
625				630						635					640	
atc	cat	gat	gga	aaa	ggt	aag	cac	aat	ggt	cag	att	tgg	gtg	ttg	gaa	1968
Ile	His	Asp	Gly	Lys	Val	Lys	His	Asn	Gly	Gln	Ile	Trp	Val	Leu	Glu	
			645						650					655		
aat	gac	agg	tgc	tct	gtg	tgc	tca	tgt	cag	aat	gga	ttc	ggt	atg	tgt	2016
Asn	Asp	Arg	Cys	Ser	Val	Cys	Ser	Cys	Gln	Asn	Gly	Phe	Val	Met	Cys	
			660					665					670			
cga	cgg	atg	gtc	tgt	gac	tgt	gag	aat	ccc	aca	ggt	gat	ctt	ttt	tgc	2064
Arg	Arg	Met	Val	Cys	Asp	Cys	Glu	Asn	Pro	Thr	Val	Asp	Leu	Phe	Cys	
		675					680					685				
tgc	cct	gaa	tgt	gac	cca	agg	ctt	agt	agt	cag	tgc	ctc	cat	caa	aat	2112
Cys	Pro	Glu	Cys	Asp	Pro	Arg	Leu	Ser	Ser	Gln	Cys	Leu	His	Gln	Asn	
	690					695					700					
ggg	gaa	act	ttg	tat	aac	agt	ggt	gac	acc	tgg	gtc	cag	aat	tgt	caa	2160
Gly	Glu	Thr	Leu	Tyr	Asn	Ser	Gly	Asp	Thr	Trp	Val	Gln	Asn	Cys	Gln	
705					710					715					720	
cag	tgc	cgc	tgc	ttg	caa	ggg	gaa	ggt	gat	tgt	tgg	ccc	ctg	cct	tgc	2208
Gln	Cys	Arg	Cys	Leu	Gln	Gly	Glu	Val	Asp	Cys	Trp	Pro	Leu	Pro	Cys	
			725					730						735		
cca	gat	gtg	gag	tgt	gaa	ttc	agc	att	ctc	cca	gag	aat	gag	tgc	tgc	2256
Pro	Asp	Val	Glu	Cys	Glu	Phe	Ser	Ile	Leu	Pro	Glu	Asn	Glu	Cys	Cys	
			740					745					750			
ccg	cgc	tgt	gtc	aca	gac	cct	tgc	cag	gct	gac	acc	atc	cgc	aat	gac	2304
Pro	Arg	Cys	Val	Thr	Asp	Pro	Cys	Gln	Ala	Asp	Thr	Ile	Arg	Asn	Asp	
		755					760					765				
atc	acc	aag	act	tgc	ctg	gac	gaa	atg	aat	gtg	ggt	cgc	ttc	acc	ggg	2352
Ile	Thr	Lys	Thr	Cys	Leu	Asp	Glu	Met	Asn	Val	Val	Arg	Phe	Thr	Gly	
		770				775					780					
tcc	tct	tgg	atc	aaa	cat	ggc	act	gag	tgt	act	ctc	tgc	cag	tgc	aag	2400
Ser	Ser	Trp	Ile	Lys	His	Gly	Thr	Glu	Cys	Thr	Leu	Cys	Gln	Cys	Lys	
					790					795					800	
aat	ggc	cac	atc	tgt	tgc	tca	gtg	gat	cca	cag	tgc	ctt	cag	gaa	ctg	2448

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Asn Gly His Ile Cys Cys Ser Val Asp Pro Gln Cys Leu Gln Glu Leu  
805 810 815

tga 2451  
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<211> LENGTH: 816  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu  
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Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val  
20 25 30

Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val  
35 40 45

Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro  
50 55 60

Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys  
65 70 75 80

Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr  
85 90 95

His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg  
100 105 110

Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Val Arg Leu His  
115 120 125

Tyr Arg Ser Gly Ser His Arg Pro His Thr Glu Val Phe Pro Tyr Ile  
130 135 140

Leu Ala Asp Asp Lys Trp His Lys Leu Ser Leu Ala Ile Ser Ala Ser  
145 150 155 160

His Leu Ile Leu His Ile Asp Cys Asn Lys Ile Tyr Glu Arg Val Val  
165 170 175

Glu Lys Pro Ser Thr Asp Leu Pro Leu Gly Thr Thr Phe Trp Leu Gly  
180 185 190

Gln Arg Asn Asn Ala His Gly Tyr Phe Lys Gly Ile Met Gln Asp Val  
195 200 205

Gln Leu Leu Val Met Pro Gln Gly Phe Ile Ala Gln Cys Pro Asp Leu  
210 215 220

Asn Arg Thr Cys Pro Thr Cys Asn Asp Phe His Gly Leu Val Gln Lys  
225 230 235 240

Ile Met Glu Leu Gln Asp Ile Leu Ala Lys Thr Ser Ala Lys Leu Ser  
245 250 255

Arg Ala Glu Gln Arg Met Asn Arg Leu Asp Gln Cys Tyr Cys Glu Arg  
260 265 270

Thr Cys Thr Met Lys Gly Thr Thr Tyr Arg Glu Phe Glu Ser Trp Ile  
275 280 285

Asp Gly Cys Lys Asn Cys Thr Cys Leu Asn Gly Thr Ile Gln Cys Glu  
290 295 300

Thr Leu Ile Cys Pro Asn Pro Asp Cys Pro Leu Lys Ser Ala Leu Ala  
305 310 315 320

Tyr Val Asp Gly Lys Cys Cys Lys Glu Cys Lys Ser Ile Cys Gln Phe  
325 330 335

Gln Gly Arg Thr Tyr Phe Glu Gly Glu Arg Asn Thr Val Tyr Ser Ser  
340 345 350

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Ser Gly Val Cys Val Leu Tyr Glu Cys Lys Asp Gln Thr Met Lys Leu  
 355 360 365

Val Glu Ser Ser Gly Cys Pro Ala Leu Asp Cys Pro Glu Ser His Gln  
 370 375 380

Ile Thr Leu Ser His Ser Cys Cys Lys Val Cys Lys Gly Tyr Asp Phe  
 385 390 395 400

Cys Ser Glu Arg His Asn Cys Met Glu Asn Ser Ile Cys Arg Asn Leu  
 405 410 415

Asn Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg Ala Leu Arg  
 420 425 430

Glu Asp Asn Ala Tyr Cys Glu Asp Ile Asp Glu Cys Ala Glu Gly Arg  
 435 440 445

His Tyr Cys Arg Glu Asn Thr Met Cys Val Asn Thr Pro Gly Ser Phe  
 450 455 460

Met Cys Ile Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys  
 465 470 475 480

Thr Glu His Asp Glu Cys Ile Thr Asn Gln His Asn Cys Asp Glu Asn  
 485 490 495

Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val Cys Lys Pro  
 500 505 510

Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys Lys Asp Gly  
 515 520 525

Cys Arg Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys Ala Cys Pro  
 530 535 540

Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp Glu Cys Ser  
 545 550 555 560

Asp Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile Asn Leu Pro  
 565 570 575

Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp Asn Gly Met  
 580 585 590

Phe Ser Pro Ser Gly Glu Ser Cys Glu Asp Ile Asp Glu Cys Gly Thr  
 595 600 605

Gly Arg His Ser Cys Ala Asn Asp Thr Ile Cys Phe Asn Leu Asp Gly  
 610 615 620

Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr Gly Asp Cys  
 625 630 635 640

Ile His Asp Gly Lys Val Lys His Asn Gly Gln Ile Trp Val Leu Glu  
 645 650 655

Asn Asp Arg Cys Ser Val Cys Ser Cys Gln Asn Gly Phe Val Met Cys  
 660 665 670

Arg Arg Met Val Cys Asp Cys Glu Asn Pro Thr Val Asp Leu Phe Cys  
 675 680 685

Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu His Gln Asn  
 690 695 700

Gly Glu Thr Leu Tyr Asn Ser Gly Asp Thr Trp Val Gln Asn Cys Gln  
 705 710 715 720

Gln Cys Arg Cys Leu Gln Gly Glu Val Asp Cys Trp Pro Leu Pro Cys  
 725 730 735

Pro Asp Val Glu Cys Glu Phe Ser Ile Leu Pro Glu Asn Glu Cys Cys  
 740 745 750

Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp  
 755 760 765

Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg Phe Thr Gly  
 770 775 780

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Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys  
785 790 795 800

Asn Gly His Ile Cys Cys Ser Val Asp Pro Gln Cys Leu Gln Glu Leu  
805 810 815

<210> SEQ ID NO 9  
<211> LENGTH: 2451  
<212> TYPE: DNA  
<213> ORGANISM: Rattus norvegicus  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)...(2451)

<400> SEQUENCE: 9

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1 5 10 15

gaa gcg gtt tgg gga ctt ggt gtg gac ccc tcc cta cag att gac gtc 96  
Glu Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val  
20 25 30

tta tca gag tta gaa ctt ggg gag tcc aca gct gga gtg cgc caa gtc 144  
Leu Ser Glu Leu Glu Leu Gly Glu Ser Thr Ala Gly Val Arg Gln Val  
35 40 45

cca gga ctg cat aat ggg acg aaa gcc ttc ctc ttc caa gat tcc ccc 192  
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Ser Pro  
50 55 60

aga agc ata aaa gca ccc att gct aca gct gag cgg ttt ttc cag aag 240  
Arg Ser Ile Lys Ala Pro Ile Ala Thr Ala Glu Arg Phe Phe Gln Lys  
65 70 75 80

ctg agg aat aaa cac gag ttc aca att ctg gtg acc ctg aaa cag atc 288  
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Ile  
85 90 95

cac tta aat tcg gga gtc att ctc tcc atc cac cac ttg gat cac agg 336  
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg  
100 105 110

tac ctg gaa ctg gaa agc agc ggc cac cgg aat gag atc aga ctg cat 384  
Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Ile Arg Leu His  
115 120 125

tac cgc tct gga act cac cgc ccg cac acg gaa gtg ttt cct tat att 432  
Tyr Arg Ser Gly Thr His Arg Pro His Thr Glu Val Phe Pro Tyr Ile  
130 135 140

ttg gct gat gcc aag tgg cac aag ctc tcc tta gcc ttc agt gcc tcc 480  
Leu Ala Asp Ala Lys Trp His Lys Leu Ser Leu Ala Phe Ser Ala Ser  
145 150 155 160

cac tta att tta cac atc gac tgc aac aag atc tat gaa cga gtg gtg 528  
His Leu Ile Leu His Ile Asp Cys Asn Lys Ile Tyr Glu Arg Val Val  
165 170 175

gaa atg cct tct aca gac ttg cct ctg ggc acc aca ttt tgg ttg gga 576  
Glu Met Pro Ser Thr Asp Leu Pro Leu Gly Thr Thr Phe Trp Leu Gly  
180 185 190

cag aga aat aac gca cac ggg tat ttt aag gga ata atg caa gat gtg 624  
Gln Arg Asn Asn Ala His Gly Tyr Phe Lys Gly Ile Met Gln Asp Val  
195 200 205

caa tta ctt gtc atg ccc cag ggg ttc atc gct cag tgc ccg gat ctt 672  
Gln Leu Leu Val Met Pro Gln Gly Phe Ile Ala Gln Cys Pro Asp Leu  
210 215 220

aat cga acc tgt cca aca tgc aac gac ttc cat ggg ctt gtg cag aaa 720  
Asn Arg Thr Cys Pro Thr Cys Asn Asp Phe His Gly Leu Val Gln Lys  
225 230 235 240

atc atg gag ctg cag gac att tta tcg aag acg tca gcc aag ttg tct 768  
Ile Met Glu Leu Gln Asp Ile Leu Ser Lys Thr Ser Ala Lys Leu Ser

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245	250	255	
aga gct gaa caa cga atg aac agg ctg gat cag tgc tac tgt gag cgg Arg Ala Glu Gln Arg Met Asn Arg Leu Asp Gln Cys Tyr Cys Glu Arg 260 265 270			816
acg tgc acc atg aag gga gcc acc tac cgg gag ttc gag tcc tgg aca Thr Cys Thr Met Lys Gly Ala Thr Tyr Arg Glu Phe Glu Ser Trp Thr 275 280 285			864
gac ggc tgc aag aac tgc aca tgc ttg aat ggg acc atc cag tgc gag Asp Gly Cys Lys Asn Cys Thr Cys Leu Asn Gly Thr Ile Gln Cys Glu 290 295 300			912
act ctg gtc tgc cct gct ccc gac tgc ccg gct aaa tgc gct cca gcg Thr Leu Val Cys Pro Ala Pro Asp Cys Pro Ala Lys Ser Ala Pro Ala 305 310 315 320			960
tac gtg gat ggc aag tgc tgt aag gag tgc aag tcc acc tgc cag ttc Tyr Val Asp Gly Lys Cys Cys Lys Glu Cys Lys Ser Thr Cys Gln Phe 325 330 335			1008
cag ggg cgg agc tac ttt gag gga gaa agg agc aca gtc ttc tca gct Gln Gly Arg Ser Tyr Phe Glu Gly Glu Arg Ser Thr Val Phe Ser Ala 340 345 350			1056
tcc gga atg tgc gtc ttg tat gaa tgc aag gat cag acc atg aag ctt Ser Gly Met Cys Val Leu Tyr Glu Cys Lys Asp Gln Thr Met Lys Leu 355 360 365			1104
gtt gag aac gcc ggc tgc ccg gct tta gat tgc ccc gag tct cat cag Val Glu Asn Ala Gly Cys Pro Ala Leu Asp Cys Pro Glu Ser His Gln 370 375 380			1152
atc gcc ttg tct cac agc tgc tgc aag gtt tgc aaa ggt tat gac ttc Ile Ala Leu Ser His Ser Cys Cys Lys Val Cys Lys Gly Tyr Asp Phe 385 390 395 400			1200
tgt tct gag aag cat aca tgc atg gag aac tca gtc tgc agg aac ctg Cys Ser Glu Lys His Thr Cys Met Glu Asn Ser Val Cys Arg Asn Leu 405 410 415			1248
aac gac agg gca gtg tgc agc tgc ccg gat ggt ttc cgg gcc ctc cgg Asn Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg Ala Leu Arg 420 425 430			1296
gag gac aat gcc tac tgt gaa gac att gac gag tgt gca gag ggg cgc Glu Asp Asn Ala Tyr Cys Glu Asp Ile Asp Glu Cys Ala Glu Gly Arg 435 440 445			1344
cat tac tgc cgt gag aac acc atg tgt gtg aac aca ccg ggc tct ttc His Tyr Cys Arg Glu Asn Thr Met Cys Val Asn Thr Pro Gly Ser Phe 450 455 460			1392
ctg tgt atc tgc caa aca ggg tac atc aga atc gac gat tac tgc tgt Leu Cys Ile Cys Gln Thr Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys 465 470 475 480			1440
acg gaa cat gac gag tgc ctc aca aac cag cac aac tgt gac gag aac Thr Glu His Asp Glu Cys Leu Thr Asn Gln His Asn Cys Asp Glu Asn 485 490 495			1488
gct ttg tgc ttt aac acc gtt gga ggt cac aac tgc gtc tgc aag cct Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val Cys Lys Pro 500 505 510			1536
ggg tac act ggg aat gga acc acg tgc aaa gct ttc tgc aaa gac ggc Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys Lys Asp Gly 515 520 525			1584
tgc aaa aac gga ggt gcc tgc att gct gcc aat gtc tgt gct tgc cca Cys Lys Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys Ala Cys Pro 530 535 540			1632
caa ggc ttc acc gga ccc agc tgt gag aca gac att gat gag tgc tct Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp Glu Cys Ser 545 550 555 560			1680
gag ggc ttt gtt cag tgt gac agc cgt gcc aac tgc att aac ctg cct Glu Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile Asn Leu Pro			1728

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565	570	575	
ggg tgg tac cac tgt gag tgc aga gat ggc tac cat gac aat ggg atg Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp Asn Gly Met 580 585 590			1776
ttt gcg cca ggt gga gaa tcc tgt gaa gat att gat gaa tgt ggg act Phe Ala Pro Gly Gly Glu Ser Cys Glu Asp Ile Asp Glu Cys Gly Thr 595 600 605			1824
ggg agg cac agc tgt gcc aat gac acc att tgc ttc aac ttg gac ggt Gly Arg His Ser Cys Ala Asn Asp Thr Ile Cys Phe Asn Leu Asp Gly 610 615 620			1872
ggc tac gat tgc cgg tgt ccc cat gga aag aac tgc aca ggg gac tgc Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr Gly Asp Cys 625 630 635 640			1920
gtg cac gac ggg aaa gtc aaa cac aac ggc cag atc tgg gtg ctg gag Val His Asp Gly Lys Val Lys His Asn Gly Gln Ile Trp Val Leu Glu 645 650 655			1968
aac gac agg tgc tct gtg tgt tcc tgc cag act gga ttt gtt atg tgc Asn Asp Arg Cys Ser Val Cys Ser Cys Gln Thr Gly Phe Val Met Cys 660 665 670			2016
caa cgg atg gtc tgt gac tgc gaa aac ccc aca gtt gac ctc tcc tgc Gln Arg Met Val Cys Asp Cys Glu Asn Pro Thr Val Asp Leu Ser Cys 675 680 685			2064
tgc cct gag tgc gac cca agg ctg agc agc cag tgc ctg cat caa aac Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu His Gln Asn 690 695 700			2112
ggg gaa acc gtg tac aac agc ggt gac acc tgg gcc cag gat tgc cgt Gly Glu Thr Val Tyr Asn Ser Gly Asp Thr Trp Ala Gln Asp Cys Arg 705 710 715 720			2160
cag tgc cgc tgc ttg caa gaa gaa gtt gac tgc tgg ccc ctg gct tgc Gln Cys Arg Cys Leu Gln Glu Glu Val Asp Cys Trp Pro Leu Ala Cys 725 730 735			2208
cca gag gta gag tgt gaa ttt agt gtc ctt cct gag aac gag tgc tgc Pro Glu Val Glu Cys Glu Phe Ser Val Leu Pro Glu Asn Glu Cys Cys 740 745 750			2256
cca cgc tgt gtc acc gat cct tgt cag gct gac acc atc cgc aat gac Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp 755 760 765			2304
atc acc aaa acc tgc ctg gac gag atg aac gtg gtt cgc ttc act ggg Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg Phe Thr Gly 770 775 780			2352
tct tcc tgg atc aag cac ggc acg gag tgc acc ctc tgc cag tgc aag Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys 785 790 795 800			2400
aac ggc cac gtg tgc tgc tca gtg gac cca cag tgc ctc cag gag ctg Asn Gly His Val Cys Cys Ser Val Asp Pro Gln Cys Leu Gln Glu Leu 805 810 815			2448
tga *			2451

&lt;210&gt; SEQ ID NO 10

&lt;211&gt; LENGTH: 816

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Rattus norvegicus

&lt;400&gt; SEQUENCE: 10

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Glu Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val  
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Leu Ser Glu Leu Glu Leu Gly Glu Ser Thr Ala Gly Val Arg Gln Val

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65					70					75					80
Leu	Arg	Asn	Lys	His	Glu	Phe	Thr	Ile	Leu	Val	Thr	Leu	Lys	Gln	Ile
				85					90					95	
His	Leu	Asn	Ser	Gly	Val	Ile	Leu	Ser	Ile	His	His	Leu	Asp	His	Arg
			100					105					110		
Tyr	Leu	Glu	Leu	Glu	Ser	Ser	Gly	His	Arg	Asn	Glu	Ile	Arg	Leu	His
		115					120					125			
Tyr	Arg	Ser	Gly	Thr	His	Arg	Pro	His	Thr	Glu	Val	Phe	Pro	Tyr	Ile
	130					135					140				
Leu	Ala	Asp	Ala	Lys	Trp	His	Lys	Leu	Ser	Leu	Ala	Phe	Ser	Ala	Ser
145					150					155					160
His	Leu	Ile	Leu	His	Ile	Asp	Cys	Asn	Lys	Ile	Tyr	Glu	Arg	Val	Val
				165					170					175	
Glu	Met	Pro	Ser	Thr	Asp	Leu	Pro	Leu	Gly	Thr	Thr	Phe	Trp	Leu	Gly
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Gln	Arg	Asn	Asn	Ala	His	Gly	Tyr	Phe	Lys	Gly	Ile	Met	Gln	Asp	Val
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Gln	Leu	Leu	Val	Met	Pro	Gln	Gly	Phe	Ile	Ala	Gln	Cys	Pro	Asp	Leu
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Asn	Arg	Thr	Cys	Pro	Thr	Cys	Asn	Asp	Phe	His	Gly	Leu	Val	Gln	Lys
225					230					235					240
Ile	Met	Glu	Leu	Gln	Asp	Ile	Leu	Ser	Lys	Thr	Ser	Ala	Lys	Leu	Ser
				245					250					255	
Arg	Ala	Glu	Gln	Arg	Met	Asn	Arg	Leu	Asp	Gln	Cys	Tyr	Cys	Glu	Arg
		260						265					270		
Thr	Cys	Thr	Met	Lys	Gly	Ala	Thr	Tyr	Arg	Glu	Phe	Glu	Ser	Trp	Thr
		275					280					285			
Asp	Gly	Cys	Lys	Asn	Cys	Thr	Cys	Leu	Asn	Gly	Thr	Ile	Gln	Cys	Glu
	290					295					300				
Thr	Leu	Val	Cys	Pro	Ala	Pro	Asp	Cys	Pro	Ala	Lys	Ser	Ala	Pro	Ala
305					310					315					320
Tyr	Val	Asp	Gly	Lys	Cys	Cys	Lys	Glu	Cys	Lys	Ser	Thr	Cys	Gln	Phe
				325					330					335	
Gln	Gly	Arg	Ser	Tyr	Phe	Glu	Gly	Glu	Arg	Ser	Thr	Val	Phe	Ser	Ala
			340					345					350		
Ser	Gly	Met	Cys	Val	Leu	Tyr	Glu	Cys	Lys	Asp	Gln	Thr	Met	Lys	Leu
		355					360					365			
Val	Glu	Asn	Ala	Gly	Cys	Pro	Ala	Leu	Asp	Cys	Pro	Glu	Ser	His	Gln
	370					375					380				
Ile	Ala	Leu	Ser	His	Ser	Cys	Cys	Lys	Val	Cys	Lys	Gly	Tyr	Asp	Phe
385					390					395					400
Cys	Ser	Glu	Lys	His	Thr	Cys	Met	Glu	Asn	Ser	Val	Cys	Arg	Asn	Leu
				405					410					415	
Asn	Asp	Arg	Ala	Val	Cys	Ser	Cys	Arg	Asp	Gly	Phe	Arg	Ala	Leu	Arg
			420					425					430		
Glu	Asp	Asn	Ala	Tyr	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Ala	Glu	Gly	Arg
		435					440					445			
His	Tyr	Cys	Arg	Glu	Asn	Thr	Met	Cys	Val	Asn	Thr	Pro	Gly	Ser	Phe
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Leu Cys Ile Cys Gln Thr Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys  
 465 470 475 480  
 Thr Glu His Asp Glu Cys Leu Thr Asn Gln His Asn Cys Asp Glu Asn  
 485 490 495  
 Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val Cys Lys Pro  
 500 505 510  
 Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys Lys Asp Gly  
 515 520 525  
 Cys Lys Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys Ala Cys Pro  
 530 535 540  
 Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp Glu Cys Ser  
 545 550 555 560  
 Glu Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile Asn Leu Pro  
 565 570 575  
 Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp Asn Gly Met  
 580 585 590  
 Phe Ala Pro Gly Gly Glu Ser Cys Glu Asp Ile Asp Glu Cys Gly Thr  
 595 600 605  
 Gly Arg His Ser Cys Ala Asn Asp Thr Ile Cys Phe Asn Leu Asp Gly  
 610 615 620  
 Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr Gly Asp Cys  
 625 630 635 640  
 Val His Asp Gly Lys Val Lys His Asn Gly Gln Ile Trp Val Leu Glu  
 645 650 655  
 Asn Asp Arg Cys Ser Val Cys Ser Cys Gln Thr Gly Phe Val Met Cys  
 660 665 670  
 Gln Arg Met Val Cys Asp Cys Glu Asn Pro Thr Val Asp Leu Ser Cys  
 675 680 685  
 Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu His Gln Asn  
 690 695 700  
 Gly Glu Thr Val Tyr Asn Ser Gly Asp Thr Trp Ala Gln Asp Cys Arg  
 705 710 715 720  
 Gln Cys Arg Cys Leu Gln Glu Glu Val Asp Cys Trp Pro Leu Ala Cys  
 725 730 735  
 Pro Glu Val Glu Cys Glu Phe Ser Val Leu Pro Glu Asn Glu Cys Cys  
 740 745 750  
 Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp  
 755 760 765  
 Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg Phe Thr Gly  
 770 775 780  
 Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys  
 785 790 795 800  
 Asn Gly His Val Cys Cys Ser Val Asp Pro Gln Cys Leu Gln Glu Leu  
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<210> SEQ ID NO 11  
 <211> LENGTH: 2460  
 <212> TYPE: DNA  
 <213> ORGANISM: Mus musculus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1) ... (2460)  
 <221> NAME/KEY: misc\_feature  
 <222> LOCATION: (1) ... (2460)  
 <223> OTHER INFORMATION: n = A, T, C or G

<400> SEQUENCE: 11

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Leu Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln	
20 25 30	
att gac gtc tta aca gag tta gaa ctt ggg gag tct aca gat gga gtg	144
Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Asp Gly Val	
35 40 45	
cgc caa gtc ccg gga ctg cat aat ggg acg aaa gcc ttc ctc ttc caa	192
Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln	
50 55 60	
gag tcc ccc aga agc ata aag gca tcc act gct aca gct gag cgg ttt	240
Glu Ser Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Arg Phe	
65 70 75 80	
ctc cag aag ctg aga aat aaa cac gag ttc aca atc ttg gtg acc tta	288
Leu Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu	
85 90 95	
aaa cag atc cac tta aat tcg gga gtt atc ctc tcc atc cac cac ttg	336
Lys Gln Ile His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu	
100 105 110	
gat cac agg tac ctg gaa ctg gaa agc agt ggc cat cgg aat gag atc	384
Asp His Arg Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Ile	
115 120 125	
aga ctc cac tac cgc tct ggc act cac cgc ccc cac acg gaa gtg ttt	432
Arg Leu His Tyr Arg Ser Gly Thr His Arg Pro His Thr Glu Val Phe	
130 135 140	
cct tat att ttg gct gat gcc aag tgg cac aag ctc tcc tta gcc ttc	480
Pro Tyr Ile Leu Ala Asp Ala Lys Trp His Lys Leu Ser Leu Ala Phe	
145 150 155 160	
agt gcc tct cac tta att tta cac atc gac tgc aat aag atc tat gaa	528
Ser Ala Ser His Leu Ile Leu His Ile Asp Cys Asn Lys Ile Tyr Glu	
165 170 175	
cga gtg gtg gaa atg ccc ttc aca gac ttg gct ctg ggc aca aca ttt	576
Arg Val Val Glu Met Pro Phe Thr Asp Leu Ala Leu Gly Thr Thr Phe	
180 185 190	
tgg ttg gga cag aga aat aat gca cat ggc tat ttt aag gga ata atg	624
Trp Leu Gly Gln Arg Asn Asn Ala His Gly Tyr Phe Lys Gly Ile Met	
195 200 205	
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Gln Asp Val His Val Leu Val Met Pro Gln Gly Phe Ile Ala Gln Cys	
210 215 220	
ccg gac ctt aat cga acc tgt cca aca tgc aac gac ttc cat ggg ctt	720
Pro Asp Leu Asn Arg Thr Cys Pro Thr Cys Asn Asp Phe His Gly Leu	
225 230 235 240	
gtg cag aaa atc atg gag ctg cag gac att tta tca aag acg tca gcc	768
Val Gln Lys Ile Met Glu Leu Gln Asp Ile Leu Ser Lys Thr Ser Ala	
245 250 255	
aag ctg tcc cga gct gaa caa aga atg aac agg ctg gat cag tgc tac	816
Lys Leu Ser Arg Ala Glu Gln Arg Met Asn Arg Leu Asp Gln Cys Tyr	
260 265 270	
tgt gag cgg aca tgc act gtg aag gga acc acc tac cga gag tct gag	864
Cys Glu Arg Thr Cys Thr Val Lys Gly Thr Thr Tyr Arg Glu Ser Glu	
275 280 285	
tcc tgg aca gac ggc tgt aag aac tgc aca tgc ttg aac ggg acc atc	912
Ser Trp Thr Asp Gly Cys Lys Asn Cys Thr Cys Leu Asn Gly Thr Ile	
290 295 300	
cag tgc gag act ctg gtc tgc cct gct cct gac tgc cct cct aaa tcg	960
Gln Cys Glu Thr Leu Val Cys Pro Ala Pro Asp Cys Pro Pro Lys Ser	
305 310 315 320	

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gcc cct gcg tat gtg gat ggc aag tgc tgt aag gag tgc aaa tca acc	1008
Ala Pro Ala Tyr Val Asp Gly Lys Cys Cys Lys Glu Cys Lys Ser Thr	
325 330 335	
tgc cag ttc cag gga cgg agc tac ttt gag gga gaa agg aac acg gca	1056
Cys Gln Phe Gln Gly Arg Ser Tyr Phe Glu Gly Glu Arg Asn Thr Ala	
340 345 350	
tac tca tct tct gga atg tgt gtc tta tat gaa tgc aag gat cag acc	1104
Tyr Ser Ser Ser Gly Met Cys Val Leu Tyr Glu Cys Lys Asp Gln Thr	
355 360 365	
atg aag ctt gtt gag aac att ggc tgc cca ccc tta gat tgt ccc gag	1152
Met Lys Leu Val Glu Asn Ile Gly Cys Pro Pro Leu Asp Cys Pro Glu	
370 375 380	
tct cat cag att gcc ttg tct cac agc tgc tgc aag gtt tgt aaa ggt	1200
Ser His Gln Ile Ala Leu Ser His Ser Cys Cys Lys Val Cys Lys Gly	
385 390 395 400	
tat gac ttc tgt tct gag aag cat acc tgc atg gag aac tcg gtc tgc	1248
Tyr Asp Phe Cys Ser Glu Lys His Thr Cys Met Glu Asn Ser Val Cys	
405 410 415	
agg aac ctg aac gac agg gtt gtg tgc agc tgc agg gat ggt ttt cgg	1296
Arg Asn Leu Asn Asp Arg Val Val Cys Ser Cys Arg Asp Gly Phe Arg	
420 425 430	
gct ctc cga gag gac aac gcc tac tgt gaa gac att gac gag tgt gca	1344
Ala Leu Arg Glu Asp Asn Ala Tyr Cys Glu Asp Ile Asp Glu Cys Ala	
435 440 445	
gaa ggg cgc cat tac tgc cgt gag aac acc atg tgt gtg aat aca cct	1392
Glu Gly Arg His Tyr Cys Arg Glu Asn Thr Met Cys Val Asn Thr Pro	
450 455 460	
ggt tct ttc atg tgt gtc tgc aaa act ggg tac atc agg atc gac gat	1440
Gly Ser Phe Met Cys Val Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp	
465 470 475 480	
tac tca tgt aca gaa cat gat gag tgt ctc aca acc cag cac aat tgt	1488
Tyr Ser Cys Thr Glu His Asp Glu Cys Leu Thr Thr Gln His Asn Cys	
485 490 495	
gat gaa aac gct ttg tgc ttt aac act gtt gga gga cac aac tgt gtc	1536
Asp Glu Asn Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val	
500 505 510	
tgc aag cct ggc tac acc ggg aat gga acc acg tgc aaa gct ttc tgc	1584
Cys Lys Pro Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys	
515 520 525	
aaa gat ggc tgt aga aac gga gga gcg tgc att gct gcc aat gtg tgt	1632
Lys Asp Gly Cys Arg Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys	
530 535 540	
gcc tgc cca caa ggc ttc acg gga ccc agc tgt gag aca gac att gac	1680
Ala Cys Pro Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp	
545 550 555 560	
gag tgc tct gag ggc ttt gtt cag tgt gac agc cgt gcc aac tgc atc	1728
Glu Cys Ser Glu Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile	
565 570 575	
aac ctg cct ggg tgg tat cac tgt gag tgc aga gac ggc tac cat gac	1776
Asn Leu Pro Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp	
580 585 590	
aat ggg atg ttt gcg cca ggc gga gaa tcc tgt gaa gat att gac gaa	1824
Asn Gly Met Phe Ala Pro Gly Gly Glu Ser Cys Glu Asp Ile Asp Glu	
595 600 605	
tgc ggg act ggg agg cac agc tgc acc aac gac acc att tgc ttc aac	1872
Cys Gly Thr Gly Arg His Ser Cys Thr Asn Asp Thr Ile Cys Phe Asn	
610 615 620	
ttg gac ggg gga tac gat tgc cgg tgt ccc cat ggg aag aac tgc act	1920
Leu Asp Gly Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr	
625 630 635 640	

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Gly Asp Cys Val His Glu Gly Lys Val Lys His Thr Gly Gln Ile Trp	
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gtg ctg gaa aac gac agg tgc tcc gtg tgt tcc tgg cag act ggg ttt	2016
Val Leu Glu Asn Asp Arg Cys Ser Val Cys Ser Trp Gln Thr Gly Phe	
660 665 670	
gtc atg tgt cga cgg atg gtc tgc gac tgc gaa aac ccc aca gat gac	2064
Val Met Cys Arg Arg Met Val Cys Asp Cys Glu Asn Pro Thr Asp Asp	
675 680 685	
ctt tcc tgc tgc cct gag tgt gac cca agg ctg agc agt cag tgc ctg	2112
Leu Ser Cys Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu	
690 695 700	
cat caa aac ggg gaa acc gtg tac aac agc ggc gac acc tgg gtc cag	2160
His Gln Asn Gly Glu Thr Val Tyr Asn Ser Gly Asp Thr Trp Val Gln	
705 710 715 720	
gat tgc cgt cag tgc cgc tgc ttg caa gga gaa gtt gac tgt tgg ccc	2208
Asp Cys Arg Gln Cys Arg Cys Leu Gln Gly Glu Val Asp Cys Trp Pro	
725 730 735	
ctg gct tgc cca gag gta gaa tgt gaa ttt agc gtc ctt cct gag aac	2256
Leu Ala Cys Pro Glu Val Glu Cys Glu Phe Ser Val Leu Pro Glu Asn	
740 745 750	
gag tgc tgc cca cgc tgt gtc acc gat cct tgt cag gcc gac acc atc	2304
Glu Cys Cys Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile	
755 760 765	
cgc aat gac atc acc aaa acc tgc ctg gac gag atg aac gtg gtt cgc	2352
Arg Asn Asp Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg	
770 775 780	
ttc acc ggg tct tcc tgg atc aag cac ggc acg gag tgt acc ctc tgc	2400
Phe Thr Gly Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys	
785 790 795 800	
cag tgc aag aat ggc cat ttg tgc tgc tca gtg gat cca cag tgc ctt	2448
Gln Cys Lys Asn Gly His Leu Cys Cys Ser Val Asp Pro Gln Cys Leu	
805 810 815	
cag gag ctg tga	2460
Gln Glu Leu *	

&lt;210&gt; SEQ ID NO 12

&lt;211&gt; LENGTH: 819

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Mus musculus

&lt;400&gt; SEQUENCE: 12

Met His Ala Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Val Ile	
1 5 10 15	
Leu Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln	
20 25 30	
Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Asp Gly Val	
35 40 45	
Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln	
50 55 60	
Glu Ser Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Arg Phe	
65 70 75 80	
Leu Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu	
85 90 95	
Lys Gln Ile His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu	
100 105 110	
Asp His Arg Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Ile	
115 120 125	
Arg Leu His Tyr Arg Ser Gly Thr His Arg Pro His Thr Glu Val Phe	

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130					135					140					
Pro	Tyr	Ile	Leu	Ala	Asp	Ala	Lys	Trp	His	Lys	Leu	Ser	Leu	Ala	Phe
145					150					155					160
Ser	Ala	Ser	His	Leu	Ile	Leu	His	Ile	Asp	Cys	Asn	Lys	Ile	Tyr	Glu
				165					170					175	
Arg	Val	Val	Glu	Met	Pro	Phe	Thr	Asp	Leu	Ala	Leu	Gly	Thr	Thr	Phe
			180					185						190	
Trp	Leu	Gly	Gln	Arg	Asn	Asn	Ala	His	Gly	Tyr	Phe	Lys	Gly	Ile	Met
		195					200					205			
Gln	Asp	Val	His	Val	Leu	Val	Met	Pro	Gln	Gly	Phe	Ile	Ala	Gln	Cys
	210					215					220				
Pro	Asp	Leu	Asn	Arg	Thr	Cys	Pro	Thr	Cys	Asn	Asp	Phe	His	Gly	Leu
225					230					235					240
Val	Gln	Lys	Ile	Met	Glu	Leu	Gln	Asp	Ile	Leu	Ser	Lys	Thr	Ser	Ala
				245					250					255	
Lys	Leu	Ser	Arg	Ala	Glu	Gln	Arg	Met	Asn	Arg	Leu	Asp	Gln	Cys	Tyr
			260					265					270		
Cys	Glu	Arg	Thr	Cys	Thr	Val	Lys	Gly	Thr	Thr	Tyr	Arg	Glu	Ser	Glu
		275					280					285			
Ser	Trp	Thr	Asp	Gly	Cys	Lys	Asn	Cys	Thr	Cys	Leu	Asn	Gly	Thr	Ile
	290					295					300				
Gln	Cys	Glu	Thr	Leu	Val	Cys	Pro	Ala	Pro	Asp	Cys	Pro	Pro	Lys	Ser
305					310					315					320
Ala	Pro	Ala	Tyr	Val	Asp	Gly	Lys	Cys	Cys	Lys	Glu	Cys	Lys	Ser	Thr
				325					330					335	
Cys	Gln	Phe	Gln	Gly	Arg	Ser	Tyr	Phe	Glu	Gly	Glu	Arg	Asn	Thr	Ala
			340					345					350		
Tyr	Ser	Ser	Ser	Gly	Met	Cys	Val	Leu	Tyr	Glu	Cys	Lys	Asp	Gln	Thr
		355					360					365			
Met	Lys	Leu	Val	Glu	Asn	Ile	Gly	Cys	Pro	Pro	Leu	Asp	Cys	Pro	Glu
	370					375					380				
Ser	His	Gln	Ile	Ala	Leu	Ser	His	Ser	Cys	Cys	Lys	Val	Cys	Lys	Gly
385					390					395					400
Tyr	Asp	Phe	Cys	Ser	Glu	Lys	His	Thr	Cys	Met	Glu	Asn	Ser	Val	Cys
				405					410					415	
Arg	Asn	Leu	Asn	Asp	Arg	Val	Val	Cys	Ser	Cys	Arg	Asp	Gly	Phe	Arg
			420					425					430		
Ala	Leu	Arg	Glu	Asp	Asn	Ala	Tyr	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Ala
		435					440					445			
Glu	Gly	Arg	His	Tyr	Cys	Arg	Glu	Asn	Thr	Met	Cys	Val	Asn	Thr	Pro
	450					455					460				
Gly	Ser	Phe	Met	Cys	Val	Cys	Lys	Thr	Gly	Tyr	Ile	Arg	Ile	Asp	Asp
465					470					475					480
Tyr	Ser	Cys	Thr	Glu	His	Asp	Glu	Cys	Leu	Thr	Thr	Gln	His	Asn	Cys
				485					490					495	
Asp	Glu	Asn	Ala	Leu	Cys	Phe	Asn	Thr	Val	Gly	Gly	His	Asn	Cys	Val
			500					505					510		
Cys	Lys	Pro	Gly	Tyr	Thr	Gly	Asn	Gly	Thr	Thr	Cys	Lys	Ala	Phe	Cys
		515					520					525			
Lys	Asp	Gly	Cys	Arg	Asn	Gly	Gly	Ala	Cys	Ile	Ala	Ala	Asn	Val	Cys
	530					535					540				
Ala	Cys	Pro	Gln	Gly	Phe	Thr	Gly	Pro	Ser	Cys	Glu	Thr	Asp	Ile	Asp
545					550					555					560

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Glu Cys Ser Glu Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile  
 565 570 575

Asn Leu Pro Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp  
 580 585 590

Asn Gly Met Phe Ala Pro Gly Gly Glu Ser Cys Glu Asp Ile Asp Glu  
 595 600 605

Cys Gly Thr Gly Arg His Ser Cys Thr Asn Asp Thr Ile Cys Phe Asn  
 610 615 620

Leu Asp Gly Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr  
 625 630 635 640

Gly Asp Cys Val His Glu Gly Lys Val Lys His Thr Gly Gln Ile Trp  
 645 650 655

Val Leu Glu Asn Asp Arg Cys Ser Val Cys Ser Trp Gln Thr Gly Phe  
 660 665 670

Val Met Cys Arg Arg Met Val Cys Asp Cys Glu Asn Pro Thr Asp Asp  
 675 680 685

Leu Ser Cys Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu  
 690 695 700

His Gln Asn Gly Glu Thr Val Tyr Asn Ser Gly Asp Thr Trp Val Gln  
 705 710 715 720

Asp Cys Arg Gln Cys Arg Cys Leu Gln Gly Glu Val Asp Cys Trp Pro  
 725 730 735

Leu Ala Cys Pro Glu Val Glu Cys Glu Phe Ser Val Leu Pro Glu Asn  
 740 745 750

Glu Cys Cys Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile  
 755 760 765

Arg Asn Asp Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg  
 770 775 780

Phe Thr Gly Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys  
 785 790 795 800

Gln Cys Lys Asn Gly His Leu Cys Cys Ser Val Asp Pro Gln Cys Leu  
 805 810 815

Gln Glu Leu

<210> SEQ ID NO 13  
 <211> LENGTH: 2453  
 <212> TYPE: DNA  
 <213> ORGANISM: Gallus gallus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)...(2453)

<400> SEQUENCE: 13

atg gag tcc ggc tgc ggc tta ggc acg ctt tgc ctt ctc ctc tgc ctg	48
Met Glu Ser Gly Cys Gly Leu Gly Thr Leu Cys Leu Leu Leu Cys Leu	
1 5 10 15	
ggg cca gtc gta ggc ttc ggc gtg gac ccc tcg ctg cag atc gac gtg	96
Gly Pro Val Val Gly Phe Gly Val Asp Pro Ser Leu Gln Ile Asp Val	
20 25 30	
ctg tcc gag ctg ggg ctg ccg ggc tac gcg gcg ggc gtg cgc cag gtg	144
Leu Ser Glu Leu Gly Leu Pro Gly Tyr Ala Ala Gly Val Arg Gln Val	
35 40 45	
ccg ggg ctg cac aac ggg agc aaa gcc ttc ctc ttc cca gat act tca	192
Pro Gly Leu His Asn Gly Ser Lys Ala Phe Leu Phe Pro Asp Thr Ser	
50 55 60	
aga agt gta aag gcg tct cca gaa aca gct gaa atc ttt ttt cag aag	240
Arg Ser Val Lys Ala Ser Pro Glu Thr Ala Glu Ile Phe Phe Gln Lys	
65 70 75 80	

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ttg aga aat aaa tat gaa ttc aca atc ctg gtg acc tta aaa caa gcc	288
Leu Arg Asn Lys Tyr Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Ala	
85 90 95	
cat tta aat tca ggg gtt att ttc tct att cat cac tta gat cac agg	336
His Leu Asn Ser Gly Val Ile Phe Ser Ile His His Leu Asp His Arg	
100 105 110	
tat ctg gaa ttg gaa agc agc ggt cat cga aat gaa atc agg ttg cat	384
Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Ile Arg Leu His	
115 120 125	
tac cgt aca ggc agt cat cgc tcc cac aca gaa gta ttc cca tac atc	432
Tyr Arg Thr Gly Ser His Arg Ser His Thr Glu Val Phe Pro Tyr Ile	
130 135 140	
ctg gca gac gat aag tgg cac agg ctt tcc tta gca atc agt gcc tct	480
Leu Ala Asp Asp Lys Trp His Arg Leu Ser Leu Ala Ile Ser Ala Ser	
145 150 155 160	
cac ttg att tta cac gtg gac tgc aat aaa atc tat gaa aga gtt gtg	528
His Leu Ile Leu His Val Asp Cys Asn Lys Ile Tyr Glu Arg Val Val	
165 170 175	
gag aag ccc ttc atg gac tta cct gtg ggt aca acc ttt tgg cta gga	576
Glu Lys Pro Phe Met Asp Leu Pro Val Gly Thr Thr Phe Trp Leu Gly	
180 185 190	
cag agg aat aat gca cac ggt tat ttt aag ggc ata atg caa gat gtg	624
Gln Arg Asn Asn Ala His Gly Tyr Phe Lys Gly Ile Met Gln Asp Val	
195 200 205	
caa tta ctt gtc atg cct caa gga ttt att tct cag tgc cca gat ctt	672
Gln Leu Leu Val Met Pro Gln Gly Phe Ile Ser Gln Cys Pro Asp Leu	
210 215 220	
aat cgg aca tgc cca act tgt aat gat ttc cat gga ctt gtg cag aaa	720
Asn Arg Thr Cys Pro Thr Cys Asn Asp Phe His Gly Leu Val Gln Lys	
225 230 235 240	
att atg gaa ctg caa gac att tta gct aaa acg tca gct aag ctg tcg	768
Ile Met Glu Leu Gln Asp Ile Leu Ala Lys Thr Ser Ala Lys Leu Ser	
245 250 255	
caa gct gag cag agg atg aac aag ttg gat cag tgc tat tgt gaa agg	816
Gln Ala Glu Gln Arg Met Asn Lys Leu Asp Gln Cys Tyr Cys Glu Arg	
260 265 270	
acc tgc aca atg aaa ggc atg aca tac aga gaa ttt gaa tcc tgg aca	864
Thr Cys Thr Met Lys Gly Met Thr Tyr Arg Glu Phe Glu Ser Trp Thr	
275 280 285	
gat ggt tgt aag aac tgc act tgc atg aat ggc act gtg cag tgt gaa	912
Asp Gly Cys Lys Asn Cys Thr Cys Met Asn Gly Thr Val Gln Cys Glu	
290 295 300	
gct ttg att tgc tcc ctc tct gac tgt cca cct aat tct gcc ctg tca	960
Ala Leu Ile Cys Ser Leu Ser Asp Cys Pro Pro Asn Ser Ala Leu Ser	
305 310 315 320	
tac gtg gat ggc aag tgc tgc aaa gaa tgt caa tcg gtg tgc ata ttt	1008
Tyr Val Asp Gly Lys Cys Cys Lys Glu Cys Gln Ser Val Cys Ile Phe	
325 330 335	
gaa ggc aga acc tac ttt gaa gga caa aga gaa acg gtg tat tca agc	1056
Glu Gly Arg Thr Tyr Phe Glu Gly Gln Arg Glu Thr Val Tyr Ser Ser	
340 345 350	
tca ggg gac tgt gtt ctg ttt gag tgc aag gac cac aaa atg cag cgt	1104
Ser Gly Asp Cys Val Leu Phe Glu Cys Lys Asp His Lys Met Gln Arg	
355 360 365	
att cca aaa gac agt tgt gca act ttg aac tgc ccg gaa tct caa cag	1152
Ile Pro Lys Asp Ser Cys Ala Thr Leu Asn Cys Pro Glu Ser Gln Gln	
370 375 380	
atc cca tta tct cac agt tgc tgc aaa atc tgt aaa ggc cat gac ttt	1200
Ile Pro Leu Ser His Ser Cys Cys Lys Ile Cys Lys Gly His Asp Phe	
385 390 395 400	

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tgc act gaa gga cat aac tgt atg gag cat tct gtc tgc cga aac cta	1248
Cys Thr Glu Gly His Asn Cys Met Glu His Ser Val Cys Arg Asn Leu	
405 410 415	
gat gac aga gct gtc tgt agc tgc cga gat ggc ttc egg gcc ctt cgg	1296
Asp Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg Ala Leu Arg	
420 425 430	
gag gac aat gcc tac tgt gaa gat gtt gat gag tgt gcc gag ggg cag	1344
Glu Asp Asn Ala Tyr Cys Glu Asp Val Asp Glu Cys Ala Glu Gly Gln	
435 440 445	
cac tac tgt cgg gag aac acc atg tgt gta aat aca cca gga tcc ttc	1392
His Tyr Cys Arg Glu Asn Thr Met Cys Val Asn Thr Pro Gly Ser Phe	
450 455 460	
atg tgc atc tgc aaa aca gga tat ata cgc att gat gac tat tca tgt	1440
Met Cys Ile Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys	
465 470 475 480	
aca gag cac gat gaa tgt gta aca aac cag cac aac tgt gat gaa aat	1488
Thr Glu His Asp Glu Cys Val Thr Asn Gln His Asn Cys Asp Glu Asn	
485 490 495	
gcg cta tgt ttc aac acg gtg ggt ggg cac aac tgt gtc tgc aag ctg	1536
Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val Cys Lys Leu	
500 505 510	
ggt tac aca gga aat ggg acg gtg tgt aaa gca ttt tgc aaa gat ggg	1584
Gly Tyr Thr Gly Asn Gly Thr Val Cys Lys Ala Phe Cys Lys Asp Gly	
515 520 525	
tgc agg aat gga gga gcc tgt att gct tcc aac gtg tgt gcc tgc cca	1632
Cys Arg Asn Gly Gly Ala Cys Ile Ala Ser Asn Val Cys Ala Cys Pro	
530 535 540	
caa ggc ttc act ggc ccc agc tgt gaa act gac att gat gaa tgc tct	1680
Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp Glu Cys Ser	
545 550 555 560	
gat ggc ttt gtg cag tgt gac agc cgt gct aat tgc atc aat ctg cca	1728
Asp Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile Asn Leu Pro	
565 570 575	
ggg tgg tac cac tgt gaa tgc agg gat ggc tac cat gac aat ggg atg	1776
Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp Asn Gly Met	
580 585 590	
ttt tca cca agt gga gaa tcc tgt gaa gac att gat gaa tgt gca act	1824
Phe Ser Pro Ser Gly Glu Ser Cys Glu Asp Ile Asp Glu Cys Ala Thr	
595 600 605	
gga agg cat agc tgt gcc aat gac act gtt tgc ttt aac ctg gat ggt	1872
Gly Arg His Ser Cys Ala Asn Asp Thr Val Cys Phe Asn Leu Asp Gly	
610 615 620	
ggg tat gac tgt cga tgt cca cat ggc aag aac tgc aca gga gac tgt	1920
Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr Gly Asp Cys	
625 630 635 640	
atc cat gaa gac aaa atc aag cac aat ggt cag att tgg gtg ctg gag	1968
Ile His Glu Asp Lys Ile Lys His Asn Gly Gln Ile Trp Val Leu Glu	
645 650 655	
aac gac aga tgc tct gtc tgc tca tgc cag agt gga tac gtg atg tgc	2016
Asn Asp Arg Cys Ser Val Cys Ser Cys Gln Ser Gly Tyr Val Met Cys	
660 665 670	
cgg cga atg gtc tgt gac tgt gaa aat ccc act gtt gac ctc ttt tgc	2064
Arg Arg Met Val Cys Asp Cys Glu Asn Pro Thr Val Asp Leu Phe Cys	
675 680 685	
tgt cct gag tgt gac cca agg ctc agc agt caa tgt tta cat cag agt	2112
Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu His Gln Ser	
690 695 700	
ggg gag ctt tcc tac aac agt ggt gac tcc tgg ata caa aac tgt cag	2160
Gly Glu Leu Ser Tyr Asn Ser Gly Asp Ser Trp Ile Gln Asn Cys Gln	
705 710 715 720	



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cag tgt cgc tgc ttg caa gga gag gtt gac tgt tgg ccc tta ccg tgc	2208
Gln Cys Arg Cys Leu Gln Gly Glu Val Asp Cys Trp Pro Leu Pro Cys	
725 730 735	
cca gag gta gac tgt gag ttc agt gtc ctc cct gag aat gag tgc tgc	2256
Pro Glu Val Asp Cys Glu Phe Ser Val Leu Pro Glu Asn Glu Cys Cys	
740 745 750	
cca cgc tgt gtc act gac ccc tgc caa gcg gac acc atc cgt aat gac	2304
Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp	
755 760 765	
atc acc aaa acc tgc ctg gat gaa acc aat gtt gtt cgc ttc act gga	2352
Ile Thr Lys Thr Cys Leu Asp Glu Thr Asn Val Val Arg Phe Thr Gly	
770 775 780	
tct tct tgg att aag cat ggc aca gag tgc aca ctc tgc caa tgt aag	2400
Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys	
785 790 795 800	
aat ggc cac gtc tgt tgc tca gtg gat cca cag tgc ctt cag gaa ctg	2448
Asn Gly His Val Cys Cys Ser Val Asp Pro Gln Cys Leu Gln Glu Leu	
805 810 815	
tga ca	2453
*	

<210> SEQ ID NO 14  
 <211> LENGTH: 816  
 <212> TYPE: PRT  
 <213> ORGANISM: Gallus gallus

<400> SEQUENCE: 14

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1 5 10 15	
Gly Pro Val Val Gly Phe Gly Val Asp Pro Ser Leu Gln Ile Asp Val	
20 25 30	
Leu Ser Glu Leu Gly Leu Pro Gly Tyr Ala Ala Gly Val Arg Gln Val	
35 40 45	
Pro Gly Leu His Asn Gly Ser Lys Ala Phe Leu Phe Pro Asp Thr Ser	
50 55 60	
Arg Ser Val Lys Ala Ser Pro Glu Thr Ala Glu Ile Phe Phe Gln Lys	
65 70 75 80	
Leu Arg Asn Lys Tyr Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Ala	
85 90 95	
His Leu Asn Ser Gly Val Ile Phe Ser Ile His His Leu Asp His Arg	
100 105 110	
Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Ile Arg Leu His	
115 120 125	
Tyr Arg Thr Gly Ser His Arg Ser His Thr Glu Val Phe Pro Tyr Ile	
130 135 140	
Leu Ala Asp Asp Lys Trp His Arg Leu Ser Leu Ala Ile Ser Ala Ser	
145 150 155 160	
His Leu Ile Leu His Val Asp Cys Asn Lys Ile Tyr Glu Arg Val Val	
165 170 175	
Glu Lys Pro Phe Met Asp Leu Pro Val Gly Thr Thr Phe Trp Leu Gly	
180 185 190	
Gln Arg Asn Asn Ala His Gly Tyr Phe Lys Gly Ile Met Gln Asp Val	
195 200 205	
Gln Leu Leu Val Met Pro Gln Gly Phe Ile Ser Gln Cys Pro Asp Leu	
210 215 220	
Asn Arg Thr Cys Pro Thr Cys Asn Asp Phe His Gly Leu Val Gln Lys	
225 230 235 240	

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Ile Met Glu Leu Gln Asp Ile Leu Ala Lys Thr Ser Ala Lys Leu Ser  
 245 250 255  
 Gln Ala Glu Gln Arg Met Asn Lys Leu Asp Gln Cys Tyr Cys Glu Arg  
 260 265 270  
 Thr Cys Thr Met Lys Gly Met Thr Tyr Arg Glu Phe Glu Ser Trp Thr  
 275 280 285  
 Asp Gly Cys Lys Asn Cys Thr Cys Met Asn Gly Thr Val Gln Cys Glu  
 290 295 300  
 Ala Leu Ile Cys Ser Leu Ser Asp Cys Pro Pro Asn Ser Ala Leu Ser  
 305 310 315 320  
 Tyr Val Asp Gly Lys Cys Cys Lys Glu Cys Gln Ser Val Cys Ile Phe  
 325 330 335  
 Glu Gly Arg Thr Tyr Phe Glu Gly Gln Arg Glu Thr Val Tyr Ser Ser  
 340 345 350  
 Ser Gly Asp Cys Val Leu Phe Glu Cys Lys Asp His Lys Met Gln Arg  
 355 360 365  
 Ile Pro Lys Asp Ser Cys Ala Thr Leu Asn Cys Pro Glu Ser Gln Gln  
 370 375 380  
 Ile Pro Leu Ser His Ser Cys Cys Lys Ile Cys Lys Gly His Asp Phe  
 385 390 395 400  
 Cys Thr Glu Gly His Asn Cys Met Glu His Ser Val Cys Arg Asn Leu  
 405 410 415  
 Asp Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg Ala Leu Arg  
 420 425 430  
 Glu Asp Asn Ala Tyr Cys Glu Asp Val Asp Glu Cys Ala Glu Gly Gln  
 435 440 445  
 His Tyr Cys Arg Glu Asn Thr Met Cys Val Asn Thr Pro Gly Ser Phe  
 450 455 460  
 Met Cys Ile Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys  
 465 470 475 480  
 Thr Glu His Asp Glu Cys Val Thr Asn Gln His Asn Cys Asp Glu Asn  
 485 490 495  
 Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val Cys Lys Leu  
 500 505 510  
 Gly Tyr Thr Gly Asn Gly Thr Val Cys Lys Ala Phe Cys Lys Asp Gly  
 515 520 525  
 Cys Arg Asn Gly Gly Ala Cys Ile Ala Ser Asn Val Cys Ala Cys Pro  
 530 535 540  
 Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp Glu Cys Ser  
 545 550 555 560  
 Asp Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile Asn Leu Pro  
 565 570 575  
 Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp Asn Gly Met  
 580 585 590  
 Phe Ser Pro Ser Gly Glu Ser Cys Glu Asp Ile Asp Glu Cys Ala Thr  
 595 600 605  
 Gly Arg His Ser Cys Ala Asn Asp Thr Val Cys Phe Asn Leu Asp Gly  
 610 615 620  
 Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr Gly Asp Cys  
 625 630 635 640  
 Ile His Glu Asp Lys Ile Lys His Asn Gly Gln Ile Trp Val Leu Glu  
 645 650 655  
 Asn Asp Arg Cys Ser Val Cys Ser Cys Gln Ser Gly Tyr Val Met Cys

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660	665	670
Arg Arg Met Val Cys Asp Cys Glu Asn Pro Thr Val Asp Leu Phe Cys 675 680 685		
Cys Pro Glu Cys Asp Pro Arg Leu Ser Ser Gln Cys Leu His Gln Ser 690 695 700		
Gly Glu Leu Ser Tyr Asn Ser Gly Asp Ser Trp Ile Gln Asn Cys Gln 705 710 715 720		
Gln Cys Arg Cys Leu Gln Gly Glu Val Asp Cys Trp Pro Leu Pro Cys 725 730 735		
Pro Glu Val Asp Cys Glu Phe Ser Val Leu Pro Glu Asn Glu Cys Cys 740 745 750		
Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp 755 760 765		
Ile Thr Lys Thr Cys Leu Asp Glu Thr Asn Val Val Arg Phe Thr Gly 770 775 780		
Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys 785 790 795 800		
Asn Gly His Val Cys Cys Ser Val Asp Pro Gln Cys Leu Gln Glu Leu 805 810 815		

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We claim:

**1.** A composition for promoting cartilage formation or repair, comprising a NELL peptide, wherein the NELL peptide is in an effective amount for cartilage formation or repair, wherein the NELL peptide comprises SEQ ID NO: 2, 4, or 6 or a fragment of SEQ ID NO: 2, 4, or 6; and wherein the composition is in an implantable formulation so as to promote cartilage formation or repair.

**2.** The composition of claim 1, further comprising a second agent.

**3.** The composition of claim 1, further comprising a second agent selected from the group consisting of chondroprotective agents, anti-pain and/or anti-inflammatory agents, growth factors, cytokines, small molecules, anti-angiogenic factors and combinations thereof.

**4.** The composition of claim 1, further comprising a pharmaceutically acceptable carrier.

**5.** The composition of claim 2, further comprising a pharmaceutically acceptable carrier.

**6.** The composition of claim 1, further comprising a material that comprises a chemical gel, a physical gel, an interpenetrating network, or a crosslinker.

**7.** The composition of claim 1 in an injectable or moldable formulation that sets upon application to a site in a body part of a human being.

**8.** The composition of claim 1, further comprising a material that degrades or releases the NELL peptide in response to a stimulus.

**9.** The composition of claim 8, wherein the stimulus is selected from mechanical stimuli, light, electromagnetic field, temperature changes, pH changes, or changes of ionic strength.

**10.** The composition of claim 1, further comprising an osteochondrogenitor cell.

**11.** The composition of claim 1, further comprising an osteochondrogenitor cell selected from mesenchymal cells, fetal embryonic cells, stem cells, bone marrow cells, adipose stem cells, fibroblasts, or combinations thereof.

**12.** The composition of claim 1, further comprising a chondrogenic cell.

**13.** The composition of claim 1, wherein cartilage formation or repair is formation or repair of hyaline or tracheal cartilage, elastic cartilage, or fibrocartilage.

**14.** The composition of claim 1, formulated into a device.

**15.** The composition of claim 1, wherein the NELL peptide is in an amount effective for treating, or ameliorating a cartilage related disorder.

**16.** The composition of claim 15, wherein the cartilage related disorder is arthropathies of various joints, arthritis of various joints, internal cartilage derangements of various joints, or spinal joint and disc-related disorders.

**17.** An implant for use in the human body comprising a substrate having a surface, wherein at least a portion of the surface includes a composition according to claim 1.

**18.** An implant for use in the human body comprising a substrate having a surface, wherein at least a portion of the surface includes a composition according to claim 2.

**19.** An implant for use in the human body comprising a substrate having a surface, wherein at least a portion of the surface includes a composition according to claim 3.

**20.** An implant for use in the human body comprising a substrate having a surface, wherein at least a portion of the surface includes a composition according to claim 4.

**21.** An implant for use in the human body comprising a substrate having a surface, wherein at least a portion of the surface includes a composition according to claim 5.

**22.** An implant for use in the human body comprising a substrate having a surface, wherein at least a portion of the surface includes a composition according to claim 10.

**23.** The implant of claim 17, wherein the substrate is resorbable.

**24.** The implant of claim 17, wherein the substrate comprises collagen.

**25.** The implant of claim 18, wherein the substrate is resorbable.

**26.** The implant of claim 18, wherein the substrate comprises collagen.

**93**

27. The implant of claim 17, which is a device selected from:

an injectable/implantable device containing NELL protein with or without cells that can be directly injected or implanted into a spinal disc to promote cartilage formation;

a disc nucleus replacement device impregnated with NELL that is designed to replace the inner portion of a vertebral disc or both the inner and outer portion of a vertebral disc;

an injectable/implantable device containing NELL with or without cells that can be directly injected into various joint spaces or implanted arthroscopically or openly into various joint spaces;

**94**

an injectable/implantable device containing NELL protein with or without cells and other factors that can be directly injected/implanted into a spinal disc to promote cartilage formation;

a disc nucleus replacement device impregnated with NELL and other factors that is designed to replace the inner portion of a vertebral disc or both the inner and outer portion of a vertebral disc; or

an injectable/implantable device containing NELL and other factors with or without cells that can be directly injected into various joint spaces or implanted arthroscopically or openly into various joint spaces.

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